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; Sequence 1, Application US/10273992
; Patent No. 6664093
; GENERAL INFORMATION:
; APPLICANT: WEI, Minghui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: C1001200DIV
; CURRENT APPLICATION NUMBER: US/10/273.992
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3377
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TYPE: DNA
; ORGANISM: Human
US-10-273-992-1
Query Match 100.0%; Score 3377; DB 4; Length 3377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Patent No. 6524840  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Nehls, Michael C.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Zambrowicz, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: No. 6524840el Human Endothelin Converting  
 ; FILE REFERENCE: LEX-0043-USA  
 ; CURRENT FILING DATE: US/09/667,373  
 ; PRIOR APPLICATION NUMBER: US 60/156,102  
 ; PRIOR FILING DATE: 1999-09-24  
 ; PRIOR APPLICATION NUMBER: US 60/176,689  
 ; PRIOR FILING DATE: 2000-01-18  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2652  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-667-373-3

Query Match	64.3%	Score 2172.6;	DB 4;	Length 2652;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2175;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	371	GACTATGATGGGATTCGAAAGGGGAGCAAGACAGCTGTATGGCTCAGCAGCAGCAGTGA	430	
Db	474	GAGTGAAGTGGGATTCGAAAGGGGAGCAAGACAGCTGTATGGCTCAGCAGCAGCAGTGA	533	
QY	431	GCTGATCTTACAGAGTGCTCTCTACTAGCTGGCTGCACTGCTTCGTGGAGCTCTGTGGC	490	
Db	534	GCTGATCTTACAGAGTGCTCTCTACTAGCTGGCTGCACTGCTTCGTGGAGCTCTGTGGC	593	
QY	491	CCTTGGGGGTCAAGTACCAAGAGACCCATCCCAAGACACTGCTTCAAGAGCTTCGAT	550	
Db	594	CCTTGGGGGTCAAGTACCAAGAGACCCATCCCAAGACACTGCTTCAAGAGCTTCGAT	653	
QY	551	TGAGTGGCTGAAAAATCCTGAGAGTCCCTGGAACCGAGGGGTGAGCCCTGTGAGACTT	610	
Db	714	TTCACAGTTCTCTGTGGGGCTGGATTCGAGAGAACCCCTGCGCATGGGCGTTCTCG	773	
QY	671	CTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGAGCCATATGAAAGCACTGCTTGA	730	
Db	774	CTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGAGCCATATGAAAGCACTGCTTGA	833	

QY	731	AAACACCAACCTTCAACTCAGACAGTGAAGCTGACAGAAAGACAAGGCGCTTCTACCTATC	790
Db	834	AAACACCACTTCAACTCAGACAGTGAAGCTGACAGAAAGACAAGGCGCTTCTACCTATC	893
QY	791	TTGCTTACAGGTGAGCGCATTTGAGAGCTGGAGCCCAAGCCACTGAGAGACTCATTTGA	850
Db	894	TTGCTTACAGGTGAGCGCATTTGAGAGCTGGAGCCCAAGCCACTGAGAGACTCATTTGA	953
QY	851	GAAGATTGTGTGTTGAAACATTACGGGGCCCTGGGACCAAGACAACTTTATGAGAGTGT	910
Db	954	GAAGATTGTGTGTTGAAACATTACGGGGCCCTGGGACCAAGACAACTTTATGAGAGTGT	1013
QY	911	GAAGCAGATGACAGGAGACTTACAGGGGCAACCCATTCTTACCGGTCTACATCAGTCCGA	970
Db	1014	GAAGCAGATGACAGGAGACTTACAGGGGCAACCCATTCTTACCGGTCTACATCAGTCTGA	1073
QY	971	CTTTAAGATTCCAAACGAATGTTTATTCAGGTGACCAAGTCTGGGCTCTTTCTGGCCCTC	1030
Db	1074	CTTTAAGATTCCAAACGAATGTTTATTCAGGTGACCAAGTCTGGGCTCTTTCTGGCCCTC	1133
QY	1031	TTGGGATTACTACTTTAAACAGAACCTGGCAATGAGAAAGTGTCTACTGTCTATCTGGATTA	1090
Db	1134	TTGGGATTACTACTTTAAACAGAACCTGGCAATGAGAAAGTGTCTACTGTCTATCTGGATTA	1193
QY	1091	CATGAGAGAACTGGGGATGCTGCTGGGTGGCGGCCCACTTCCACAGAGGAGCAGATGCA	1150
Db	1194	CATGAGAGAACTGGGGATGCTGCTGGGTGGCGGCCCACTTCCACAGAGGAGCAGATGCA	1253
QY	1151	GCAGGTGCTGGAGTTTGAGATACAGCTGTCGCCAACAATCAAGTGGCCCAAGACACAGCGCG	1210
Db	1254	GCAGGTGCTGGAGTTTGAGATACAGCTGTCGCCAACAATCAAGTGGCCCAAGACACAGCGCG	1313
QY	1211	CGACGAGGAGAAATCTACCAACAAGATGAGACTTTCGAGCTGACAGGCTCTGGAGCCCTC	1270
Db	1314	CGACGAGGAGAAATCTACCAACAAGATGAGACTTTCGAGCTGACAGGCTCTGGAGCCCTC	1373
QY	1271	CATGAACTGCTTGAGTTCTGTCTTTCTTGTCTGTCAACATTGAGATTGAGTCACTGGA	1330
Db	1374	CATGAACTGCTTGAGTTCTGTCTTTCTTGTCTGTCAACATTGAGATTGAGTCACTGGA	1433
QY	1331	GCCGTGTGTGTATGAGGATGGAATTTATTTGACACAGGTGTCAAGCTCATCAACCGCAC	1390
Db	1434	GCCGTGTGTGTATGAGGATGGAATTTATTTGACACAGGTGTCAAGCTCATCAACCGCAC	1493
QY	1391	GGAACCAAGCATCTCTGAACAATTACTCTGATCTGGAACCTGGTGCAGAAAGACAACTCAAG	1450
Db	1494	GGAACCAAGCATCTCTGAACAATTACTCTGATCTGGAACCTGGTGCAGAAAGACAACTCAAG	1553
QY	1451	CTTGGACCGAGCTTTTGAATCTGCAACAAGAAAGCTGTGGAACCTCTTATGGAACCTAA	1510
Db	1554	CTTGGACCGAGCTTTTGAATCTGCAACAAGAAAGCTGTGGAACCTCTTATGGAACCTAA	1613
QY	1511	GAAGTCTCTGTGTGCGAGGTGGGACGCTGCATCTTCAACACGAGATGACGCTTGTGCTT	1570
Db	1614	GAAGTCTCTGTGTGCGAGGTGGGACGCTGCATCTTCAACACGAGATGACGCTTGTGCTT	1673
QY	1571	TGCTTTGGGGTCCCTCTTCTGTGAAGGCAAGTTTGACCGGCAAAAGCAAGAAATTGACGA	1630
Db	1674	TGCTTTGGGGTCCCTCTTCTGTGAAGGCAAGTTTGACCGGCAAAAGCAAGAAATTGACGA	1733
QY	1631	GGGGATGATCAGCGGAATTCGGGACCGGATTTGAGAGAGCCCTGGGACAGCTGTGTTGGAT	1690
Db	1734	GGGGATGATCAGCGGAATTCGGGACCGGATTTGAGAGAGCCCTGGGACAGCTGTGTTGGAT	1793
QY	1691	GGATGAGAAGACCCGACAGGACGACCAAGAGAAAGCAGATGCACTTATGATATGATTTGG	1750
Db	1794	GGATGAGAAGACCCGACAGGACGACCAAGAGAAAGCAGATGCACTTATGATATGATTTGG	1853
QY	1751	TTTTCCAGACTTTATCTCTGAGACCCCAAGAGCTGGAATGTTTATGACGGGTACGAAAT	1810
Db	1854	TTTTCCAGACTTTATCTCTGAGACCCCAAGAGCTGGAATGTTTATGACGGGTACGAAAT	1913

1811 TTCTGAAGATCTCTTCTCCAAACAGTGAATTTGACATCTCTGCGAAGGTAT 1870  
1914 TTCTGAAGATCTCTTCTCCAAACAGTGAATTTGACATCTCTGCGAAGGTAT 1973  
1871 GGGTGAACAGCTCCGAGAGCTCCGAGCGAGACAGATGAGATGACATCCCGAGACAGT 1930  
1974 GGGTGAACAGCTCCGAGAGCTCCGAGCGAGACAGATGAGATGACATCCCGAGACAGT 2033  
1931 GAATGCTTACTTCTTCTTCACTAAGATGATGATGATGATGATGATGATGATGATGAT 1990  
2034 GAATGCTTACTTCTTCTTCACTAAGATGATGATGATGATGATGATGATGATGATGAT 2093  
1991 CCGCTTCTATGCGCGAGACAGCGCGAGAGCTGAGATGATGATGATGATGATGATGAT 2050  
2094 CCGCTTCTATGCGCGAGACAGCGCGAGAGCTGAGATGATGATGATGATGATGATGAT 2153  
2051 GGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2110  
2154 GGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2213  
2111 CTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2170  
2214 CTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2273  
2171 GGAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2230  
2274 GGAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2333  
2231 GGGGAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2290  
2334 GGGGAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2393  
2291 GCTGAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2350  
2394 GCTGAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2453  
2351 CTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2410  
2454 CTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2513  
2411 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2470  
2514 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2573  
2471 CTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2530  
2574 CTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2633  
2531 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2549  
2634 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652

RESULT 4  
US-08-574-763-1  
Sequence 1, Application US/08574763  
Patent No. 5736376  
GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi  
TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING  
TITLE OF INVENTION: ENZYME-2 AND ITS USE IN ECE INHIBITOR SCREENING  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/574,763  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Cordeir, Timothy S.  
REGISTRATION NUMBER: 38,414  
REFERENCE/DOCKET NUMBER: UTD:472  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3291 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 116..2476  
US-08-574-763-1

Query Match 64.2%; Score 2169.6; DB 1; Length 3291;  
Best Local Similarity 85.3%; Pred. No. 0;  
Matches 2560; Conservative 0; Mismatches 404; Indels 38; Gaps 11;

372 ACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431  
302 AATGAGCGGAGATTCGGAAGAGAGACAGTCCCTTGGGGTGGACACCGAGCTGAG 361  
432 CTGGTCTTGAAG 491  
362 CTGGTCTTGAAG 421  
492 CTAGGGGTCAGTACCAAG 551  
422 CTGGGGGTCAGTACCAAG 481  
552 CGAGTGGCTGGAAG 611  
482 CGAGTGGCTGGAAG 541  
612 TACAGATTCCTGCTGAG 671  
542 TACAGATTCCTGCTGAG 601  
672 TGAACACCTTCAACAG 731  
602 TGAACACCTTCAACAG 661  
732 AACACACCTTCAACAG 791  
662 AACACACCTTCAACAG 721  
792 TGCTTACAGGTGAG 851  
722 TGCTTACAGGTGAG 781  
852 AAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 911  
782 AAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841  
912 AAGGAGTGAAG 971  
842 AAGGAGTGAAG 901  
972 TCTTAAGATTCGAAG 1031  
902 TCTTAAGATTCGAAG 961  
1032 CGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1091

Db	962	CGAGATTACTACCTAAAGACCGCCCAATGAGAAAGTCTTACTGCTACTGGACTAC	1021
Oy	1092	ATGAGGAACCTGGAGATCTGTGTGGGTGGCGGCCCACTCCACGAGGAGCAGATGCG	1151
Db	1022	ATGAGGAGCTGGGGATGCTGCTGGGGCGGACAGCCCACTCCACTCGGAGCAGATGCG	1081
Oy	1152	CAGGTGCTGGAGTTTGGAGTACAGCTGGCCAACTCAACATGCTCCAGAACCAAGCGCGC	1211
Db	1082	CAGGTGCTGGAGCTGGAGATACACTGCGCCAACTCAAGGTGCTCCAGAACCAAGCGCGG	1141
Oy	1212	GACGAGGAGAAAGATCTACCAACAAGATGAGCAATTTGGAGCTGACGGGCTGGGCGCC	1271
Db	1142	GATGAGGAGAAAGATTTACCAACAAGATGAGCACTCGGAGCTGCAAGCCCTGACCTCC	1201
Oy	1272	ATGACTGGCTTGAGTCTCTGTCTTTCTGTGCTGCACCATTTGAGATTGAGTGACTGAG	1331
Db	1202	ATGACTGGCTGGAGTTTCTGTCTTTCTGTGCTGACCGCTGGAGCTGGGTGATTTGAG	1261
Oy	1332	CCTGTGTGTGTGTATGGATGGAATTAATTTGACAGGTGTCAAGACTCATCAACCGCACG	1391
Db	1262	CCTGTGTGTGTGTATGGAGCGAATTAATTTGACAGGTGTGTGAACTCATCAACCGCAC	1321
Oy	1392	GAACCAAGCATCTGTGAATAATTAACCTGTATCGGAACCTGTGTCAAAAACAACCTCAAG	1451
Db	1322	GAGCCAAGTGTCTGAACAATTAATTAATCTGGAACCTGTGTACAGAAACAATTCACAGC	1381
Oy	1452	CTGACCGACGCTTTGAGTCTGTGCACAAGAGAGCTGCTGAGACCTCTATAGCACTAAG	1511
Db	1382	CTGACCGACCGTTTGAATCTGTGCACAAGAAAGCTGTGAGAACCTCTATAGCACCAAG	1441
Oy	1512	AAATCTGTGTGTGCGGAGGTGGCAGACTGTCACTTCCAAACACGAGATGACGCTTGGCTTT	1571
Db	1442	AAATCTGTGTACCCGAGGTGGCAGACTGTCACTTCCAAACCGACGATGTCTTGGCTTT	1501
Oy	1572	GCTTTGGGGTCCCTTTGTGTGAAGGCCACGTTTACCGGCAAGGAATTTGACAG	1631
Db	1502	GCTCTGGGCTCCCTTTGTGTGAAGGCCACATTTGACCGGACAGAGAAATTTGACAG	1561
Oy	1632	GGGATGATCAACGGAATCCGACCGCATTTTATAGGAGGCTCTGGGACAGCTGTTTGATG	1691
Db	1562	GGGATGATCAACGAGATCCGAGTCCGCTTTTATAGGAGGCTCTGGGACACTTGGTTGATG	1621
Oy	1692	GATGAGAAAGCCCCGACGACCCAGGAGAAAGCAGATGCACTATGATATGATTTGT	1751
Db	1622	GACGAGAAAGCCCCGACGACCCAGGAGAAAGCAGATGCACTATGATATGATTTGT	1681
Oy	1752	TTCCCAACTTATTCCTGGAGCCCAAGAGCTGTGATGATGTTTATGACGGGTACGAATT	1811
Db	1682	TTCCCGACTTATTCCTGGAGCCCAAGAGCTGTGATGATGTTTATGATGGGTATGAAGTA	1741
Oy	1812	TCTGAAGATTTCTTCTTCCAAACAATGTGTAATTTGTACAATCTCTGCGCAAGTTATG	1871
Db	1742	TCTGAAGATTTCTTCTTCCAAACAATGTGTAATTTGTACAATCTCTGCTTAAAGTATG	1801
Oy	1872	GCTGACCAAGCTCCGCAAGCTTCCAGCCGAGACCAAGTGAACATGACCCCCACAGATG	1931
Db	1802	GCTGACCAAGCTCCGCAAGCTTCCAGCCGAGACCAAGTGAACATGACCCCCACAGATG	1861
Oy	1932	AATGCTTATCTACTTCCAACTTAAGATATGATCTTCCCCGTGGCATCTTCAAGCC	1991
Db	1862	AATGCTTATCTACTTCCAACTTAAGATATGATCTTCCCCGTGGCATCTTCAAGCC	1921
Oy	1992	CCCTTCTATGCGCGCAACCAACCCAGGCGCTGAATCTGGTGGCATCGGTGTGATG	2051
Db	1922	CCCTTCTATGCACTTGCACCAACCCCGAGCCCTGAATCTGGTGGCATCGGTGTGATG	1961
Oy	2052	GGCCATGAGTTGACGATGCTTTGATGACCAAGGCGCGAGTATGACAAAGAGGAGAC	2111
Db	1982	GGCCATGAGTTGACCATGTGCTTTGATGACCAAGGCGCGAGTATGACAAAGAGGAGAT	2041
Oy	2112	CTGCGGGCTGTGTGCAAGATGAGTCTCTGGCAGCTTCCGGAACCAACGGCTGTATG	2171
Db	2042	CTGCGGGCTGTGTGCAAGATGAGTCTTGTGCAAGCTTCCGGAACCAACGGCTGTGATA	2101

QY	2172	AAGGAAACAGTACATCAATAATACAGAGTCAATAGGGGAGAGGGCTCAACGGCCGCCAGACGCTG	2231
Db	2102	GAGAGACAGTACACCCAGTACAGAGTCAACCGGGGAGAGCTCAACCGGGCCGCCAGACCTG	2161
QY	2232	GGGAGAAACATTTGCTGACCAACCGGGGGGCTGAAAGGCTCCTACATATGCTTACAAAGCATGG	2291
Db	2162	GGGGAGAAACATTTGCCGACCAATAGGGGGGGCTTAAGGCTCCTACCAACGCTTACAAAGCATGG	2221
QY	2292	CTGAGAAAGCATGGGGAGAGAGACGAACCTGCAGCCGCGGGGCTCAACCAACCAACAGCTC	2351
Db	2222	CTAAGAAAGCATYGGGGAGAGAGACAGACACTGCTAGGAGCTCAACCAACCAACAGCTC	2281
QY	2352	TTCTTTCGGGAAATTGGCCAGAGTGTGGTGCCTGGTCCGACACAGAGAGCTCAGAG	2411
Db	2282	TTCTTTTGGGAAATTGGCCAGAGTGTGGTGCCTGGTCCGACACCCAGAGAGCTCTCAGAG	2341
QY	2412	GGGCTGTGTGACCCACCCCAACAGCCCTGACCCTCTCCGCTGTGGGCACTTCTCCAAC	2471
Db	2342	GGGCTGTGTGACCCACCCCAACAGCCCTGACCCTCTCCGCTGTGGGCACTCTCTCCAAC	2401
QY	2472	TCCCGTACATTTCCCTGGGGCACTTGGGCTGCCCTGTGGGCTCCCGATGAACCAAGGGCAG	2531
Db	2402	TCCCGTACATTTCCCTGGGGCACTTGGGCTGCCCTGTGGGCTCCCGATGAACCTCAGGGCAG	2461
QY	2532	CTGTGTAGAGGTGTGTGTAGACCTGGATCAGGGGAGAAATGCCCCAGCT--GTCAACAGACC	2588
Db	2462	CTTTGTAGAGGTGTGTGTAGACCTGGGTTTGGAGAGAAATGCGACAGCTCGATTGCCAGACC	2521
QY	2589	TGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGAGAGAAACAAATGCAGCT	2648
Db	2522	TGGGGTATCTTGGCCCAACAGGCTCTGCTCTGGGGGTATATGGAAAGGCATATGCCAGCT	2581
QY	2649	GGGCTGGGATGATGACCTCCGCCCCCAACAG--GTGACATATGATATC-AGACCCCTCCATATC	2705
Db	2582	GGGCTGTGTGTCTGCCCCCTTCAACACCAATAGGTGTATCATAGTCTTATGCTTCTCTCGGCC	2641
QY	2706	ACCAATTGTGCTCTGTCTTTGGGGGTGCCCTGCTCCAGACAGGCCCAACCATTCAC	2765
Db	2642	TCCACATGTGCTCTGTCTTTGGGGGTGCCCTGCTCCAGACAGGCCCAACCATTCAC	2701
QY	2766	TGTATCAATCTTTCCGTGTACACCCGTCTGGAAAGGTCTGGG-TGGGAGGGCAGATTCCC	2824
Db	2702	TGTATCAATCTTTCCGTGTGTACACCCGTCTGGAAAGGTCTGGG-TGGGAGGGCAGATTCCC	2758
QY	2825	ATAGAGAGAGTGTGCTCTTCTGTGTCCCAAGGCTCATCTAGCTGCGGACATGGGCTCT	2884
Db	2759	ACAAGAAAGGGGTCCACCTCTTTTAGTGTCCCAAGCTCATGTGGGTTTGTGTGGCCACAGGGCT	2818
QY	2885	GCCGTGCTGCGCCCACTGTGACCAAGGCTGTGGTGTGTACTCTTGTGACTTTCTCCC	2944
Db	2819	ATTGTGTGCTG-----CTGACCAAGCAAGGGGCCCAACATATGTGCTTCCACACATCTCCCC	2873
QY	2945	-AGGCTACATCAGTGGGCACTTATAGGGGTGACATCAGTCTGTCTGAGTCAACCTCAAGG	3003
Db	2874	AAGGCTTATCTACCTGCTCCCTTTGGGCAATAGACAGAGCTCTTTTCAAGCCCTGCCCCAAGT	2933
QY	3004	CTACCCCCACCTCAACCTGTGCTCTTGTGCACTGTCTCCAGTGTGCTGTGACCTTC	3063
Db	2934	GCGACCT-----TATATTCATGTTCTCTCATGCTCACTGCTCTTAAATATGCTGCAGGCCCTC	2989
QY	3064	ACTGAC-----AGTCTCTATATGGAAGCCCAAGGGCCCTGTGAAGGCTCTCT	3108
Db	2990	TCTATACGAGACCCCTGTGCTGAGTCTTTATGTGGAAGTCCAAACAGCTTTTACAAACCTTCC	3049
QY	3109	GCT--GCCCATGTTTCCCTGAGGCTGAGAGGGGAAGTGCATATGTGTAGAGGGGTACTGTT	3166
Db	3050	TGTTTGCTTCCCAAGGCTCCTGTGGGTGACGGGGATGTGTATCATGTACAGGATGTGAGG	3109
QY	3167	TCTGTGTCTTAAAGGC-ACAAGCTTATAGCAATATGATTTCTTCCCTGTGACAAAGCAGGA	3225
Db	3110	CCCTGATCTTTGGGGTTTACAAGTCTTATAGGGGTGTACATGATTTCTCTGTGACCAAGCAGGA	3169



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QY 1792 TTTATGACGGGTACGAATTTCTGAAATCTTCTTCCAAAATGTTGATTTGACA 1851
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DB 1542 TGTATATGACTACACTGACGAGTTCAGACCTCTACTTTGAAAATGCGATGGTTTTC 1601
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QY 1852 ACTTCTGCGCAAGTTATGCTGACACAGCTCCGCAAGCTCCAGCCGACCAAGTGA 1911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1602 ACTTCTGACGAGGGTCACTGCGCATGCTCAGCAAGAGCCCAACAGATCAGTGA 1661
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QY 1912 GCATGACCCCGCAGAGTGAATGCTACTACTTCCAACTAAGATGATGCTTCC 1971
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DB 1662 GCATGACCCCGCAGAGTGAATGCTACTACTTCCAACTAAGATGATGCTTCC 1721
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QY 1972 CCGCTGCAATCTGCAAGGCCCCCTTCTATGCCCCGCAACCAAGGCCCCCTGAACTTCG 2031
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DB 1722 CCGCCGGGATCTCGAGGACCATTTCTACACAGCTTCTCAACCAAGGCCCCCTTAACTTTC 1781
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QY 2032 GTGCGATCGGTGTGTCATGAGGCGCATGATGTAAGCATGCTTTGATGACCAAGGCGCG 2091
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DB 1782 GTGCGATGAGGTGTGTCATGAGGCGCATGATGTAAGCATGCTTTGATGACCAAGGCGCG 1841
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QY 2092 AGTATGACAAAGAGGAACTGCGGCCCCCTGCGGAGAAATGAGTCCCTGCGAGCCCTTC 2151
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DB 1842 AGTATGACAAAGAGGAACTGCGGCCCCCTGCGGAGAAATGAGTCCCTGCGAGCCCTTC 1901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2152 GGAACCAACAGGCTGATGAGAGAAAGTAAATACATATACAGATCAATGAGGAGAGGCG 2211
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DB 1902 AGGCTAGACAGAGTGTATGTATGAGACATACAGCACTACAGCTGAGAGGAGAGCCGG 1961
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QY 2212 TCAACGCGCGCGCAGACGCTGCGGAGAGAACTTTCGTAACAAGGCGGCTGAGAGCTGCT 2271
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DB 1962 TGAACGCGCGCGCAGACGCTGCGGAGAGAACTTTCGTAACAAGGCGGCTGAGAGCTGCT 2021
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QY 2272 ACAATGCTTACAAAGATGCTGAGAGAAAGATGAGGAGAGAGCACTGCGAGCCGTG 2331
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DB 2022 ATCGGCTTACCAAGATGCTGAGAGAAAGATGAGGAGAGAGCACTGCGAGCCGTG 2081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2332 GGTCAACCAACAGACGCTTCTTCTGAGGATTTGCCAGGTGTGCTCGATCGCA 2391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2082 GGTCAACCAACAGACGCTTCTTCTGAGGATTTGCCAGGTGTGCTCGATCGCA 2141
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QY 2392 CACGAGAGGCTTCAAGAGGCTGTGTAACGACCCCAAGCCCTGCGCTTCGCG 2451
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DB 2142 CACGAGAGGCTTCAAGAGGCTGTGTAACGACCCCAAGCCCTGCGCTTCGCG 2201
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QY 2452 TGTGCGGCACTCTCTCAACTCCCGTGACTTCTGCGGAGCACTTGGCTGCTGTGAGCT 2511
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DB 2202 TGTGCGGCTCTCTCTCAACTCCCGTGACTTCTGCGGAGCACTTGGCTGCTGTGAGCT 2261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2512 CCCCCATGAACCAAGGAGGCTGTGAGGATGAGTA 2548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2262 CACCCATGAACCAAGGAGGCTGTGAGGATGAGTA 2298
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RESULT 6  
US-08-646-273-29

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; Sequence 29, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroege, Burhard, Seuberg, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Blard, Oter, Rainer, Subkowski, Thomas, Hilten, Heinz.
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinlauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0

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; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
; US-08-646-273-29

Query Match      29.8%; Score 1007.2; DB 3; Length 2314;
Best Local Similarity 67.9%; Pred. No. 6.5e-231;
Matches 1453; Conservative 0; Mismatches 678; Indels 9; Gaps 3;

QY 411 GGCTACGCAACGAGCTGAGCTGCTTGAAGAGTCTCTACTGCTGCTGACATG 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 168 GCGCCAGAGACCCCGGTGAGAGAGCGGCTGTGTGCTGTGCGCTCTGCGCGGCA 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 471 CTTCGGGCTGCTGTGCGCTTGAAGAGTCTGATACAGAGACCCATCCACAGCAC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 TTGTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 531 TGCCTTACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 285 TGTGTAAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 591 GTGAGCGCTGTGAGAGCTTTTACAGTCTCTGTGTGAGGCTGCTGCTGCTGCTGCTG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 345 GTGAGCGCTGTGAGAGCTTTTACAGTCTCTGTGTGAGGCTGCTGCTGCTGCTGCTG 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 651 CTGCGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 405 GTGCGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 711 ATACTGAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 465 ATCATGAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 771 ACAAGCGCTTCTTACTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 522 GACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 831 CCACTGAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 582 CCGCTGATGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 891 GACAACTTATGAGAGTGTGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 642 GACAACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 702 TCCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1011 TCTGCGCTTCTTCTGCGCTTCTGCGCTTCTGCGCTTCTGCGCTTCTGCGCTTCT 1070
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DB 762 TCTGCGCTTCTTCTGCGCTTCTGCGCTTCTGCGCTTCTGCGCTTCTGCGCTTCT 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1071 CTCACTGCTTATCTGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 822 CTGAGCGAGTACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1128 ACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1187
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 882 GACACCATCGGCGCCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
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QY 1188 ACAGTGGCCCAAGGACGAGGCGGCGAGAGAGAAATCTTACCAAGATGACATTTGCG 1247
DB 942 ACCATCCCCAGAGAAAGCCCGGAGAGAACTCATCTACCAAGATGAGCGCGCT 1001
QY 1248 GAGCTGAGGCTCTGGCGCCCTTCATGAGCTGGCTTGAAGTTCTCTTCTTCTGTCGA 1307
DB 1002 GAGTTCAAGACTTTGGGCGCCCGCATCACTGGCTGCGCTTCTCAACACATCTTCAAC 1061
QY 1308 CCATTGAGATTTGAGTACTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1367
DB 1062 CCGTGTAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1121
QY 1368 GTGTCAAGCTTCATCAACGCGAGAGCAAGCATCTGTAACATTAACCTGATCTGAAAC 1427
DB 1122 GTCTCAACCTTCATCAACGAGAGCAAGCAAGATGCTGTGTGTGTGTGTGTGTGTGT 1181
QY 1428 CTGGTCAAAAGACAACTTCAGACCTGAGACCGACGCTTTGAGTCTGTCAAGAAAGCTG 1487
DB 1182 CTGGTCAAGAAAGACGAGCTCTTCTGTGATCAGCGCTTCAGAGACGCGCGAGAAAGTTC 1241
QY 1488 CTGGAAGACCTCTATGAGCACTTAAGAAAGTCTGTGTGTGTGTGTGTGTGTGTGTGT 1547
DB 1242 ATGGAAGTCAATGATGAGCAAGAAAGACGATGCTTCCCGCTGAAAGTTTGTGTGAGT 1301
QY 1548 AACACGAGATGACGCGCTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1607
DB 1302 GATACAGAGAAACCTTGGGCTTTCGCTGTGGCCCAATGTTCTTCAAGAGGACCTTCGCT 1361
QY 1608 CGGCAAGCAAGAAATTTGAGAGGGGATGATCAGCGAAATCCGAGCCGATTTGAGAG 1667
DB 1362 GAGGACAGCAAGAACATAGCCAGAGATCATCTGTGAGATCAAGAAAGGCTTTGAAAG 1421
QY 1668 GCGCTGGAGACAGCTGTTTGGATGAGTGAAGAACCCCGGAGAGCAAGAGAAAGCA 1727
DB 1422 AGCTTGAAGACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1481
QY 1728 GATGCACTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1787
DB 1482 GAGGCACTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1541
QY 1788 GATGTTTATGAGCGGATGAGAAATTTCTGAAGATTTCTTCTTCAAAACATGTTGAATTTG 1847
DB 1542 AAAGTGTCAATGATCAACCGCTGTGACAGACCTCTTCACTTCAAGAAACGCGATGCGGTTT 1601
QY 1848 TACAACTTCTGTGCAAGGTTATGCTGACCACTCCGGAAGCTCCGACCGAGACAG 1907
DB 1602 TTCAACTTCTCTGAGAGGTCACCTGCGACAGCTCCGAAAGCGCCCAAGAGATCAG 1661
QY 1908 TGAAGCATGACCCCGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1967
DB 1662 TGAAGCATGACCCCGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1721
QY 1968 TTTCCCGCTGAGTCTGAGGCGCCCTTCTTATGCGCGCAACCAACCCCAAGGCTGAGAC 2027
DB 1722 TTTCCCGGCGGAATCTGAGGCGGCAATCTTCAACCCGCTTCAACCAATGCTTTAAAC 1781
QY 2028 TTTGGTGGCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2087
DB 1782 TTTGGGCGGATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1841
QY 2088 CGGAGATGATCAAAAGAGAGAAAGCTTGGCGCCCTGAGGAGAGATGATGATGATGATGAT 2147
DB 1842 CGAGAGTACAGCAAGATGAGAACTTCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1901
QY 2148 TTTCCGAAACCAACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2207
DB 1902 TTTCAAGAGAGAGACGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1961
QY 2208 AGGCTCAACGCGCGGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2267
DB 1962 CCGGTGAACGCGCGGAGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2021
QY 2268 GCCTACAAATCTTACAAAGCATGGCTGAGAAAGCATGGGAGAGAGAGCAATGCGACGC 2327

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DB 2022 GCTATCGGGCCCTTACAGAACTGGGTCAAGAAAGATGGGGCTGAGACAGACTGCCAAC 2081
QY 2328 GTGGGCTTACCAACCAACCACTCTTCTTCTGTGGATTTGGCCAGTGTGTGTGTGTGT 2387
DB 2082 CTGGGTCTCAACCAACCAACCACTCTTCTTCTGTGGATTTGGCCAGTGTGTGTGTGT 2141
QY 2388 CGACACCAAGAGGCTCTACGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2447
DB 2142 CGGACCCCGGAGAGTTCGACAGAGGTCTCATACCGATCCCAAGCCCTCCGCTTC 2201
QY 2448 CCGGTCTGGGAGACTCTCTCAACTTCCCGTGAATTCCTGCGGCACTTGGCTGCTGTG 2507
DB 2202 CCGGTCTATGCGCTCATCTCAACTTCAAGAGAGTCTCGGAACACTTCCAGCTGCGGCC 2261
QY 2508 GCGTCCCGCATGACCCAGGAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2547
DB 2262 GCGTCAACCATGAAACCGCATCAAGATGTGAAGTCTGTGT 2301

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## RESULT 7

US-08-646-273-22

Sequence 22, Application US/08646273

Patent No. 6066502

GENERAL INFORMATION:

APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,

APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hilten, Heinz.

TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

STREET: 1101 Connecticut Avenue

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM AT-compatible, 80486 processor

OPERATING SYSTEM: MS-DOS version 6.0

SOFTWARE: WordPerfect version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,273

FILING DATE: 16-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP94/03706

FILING DATE: 11-NOV-1994

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 2129 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA for mRNA

US-08-646-273-22

Query Match 29.8%; Score 1007; DB 3; Length 2129;

Best Local Similarity 68.5%; Pred. No. 7e-231;

Matches 1436; Conservative 0; Mismatches 650; Indels 9; Gaps 3;

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QY 456 CTGCTGCTGACACTGCTTCTGAGGCTGCTTGTGCGCTTGAAGGATCCAGTACAGAGAGAC 515
DB 39 CTCTGGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 95
QY 516 CCATCCACAGACAGCTGCTTCAAGAGGCTGATTCAGTGTGAGGAGGAGAAATCTCTGAG 575
DB 96 AGAAGCGCTCGGTGTGCTTAAGTAGGCTGATCTCGGTGACAGCTCCATCTTGAAT 155
QY 576 TCCCTGAGACGAGGAGTGTGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 635
DB 156 TCCATGAGACCCAGCGGTGAGCCCTGTGACAGACTTCTTCAACCTATGCTGTGTGTGTGT 215

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OY	636	ATTGGAGGAACCCCTGCGCGATGGGGGTTCTGCTGTGGAAACA	CTTCAACAGCCTCTGG	695	
Db	216	ATCAAAGCCAAACCCCTGCGGATGGCACTGCGCGTGGGGACTT	CAGCAACTCTGG	275	
OY	696	GACCAAAACAGGCCATACTGAGACCTGCTTGA	AAACCAACCACTTCACTCCAGCAGT	755	
Db	276	GAACGACAAACAGGCATCATCAAGACCTCTTGA	AAATCCAGGCGCAGCGTAGC---	332	
OY	756	GAAGCTGAGCAGAGACACAGCGCTTCTA	CTTATTTGGCTTACAGGTGAGCGCAATTGAG	815	
Db	333	GAGGCAAGAGAGAGAACGACGAGAGTAACTTAC	CGAGCTCGCATGAACGAACACAGATTGAG	392	
OY	816	GAGCTGGGAGGCCCACTGAGAACCTCAATTGA	GAAGATTGGTGGTTGGAACTTACG	875	
Db	393	GAGCTCAAGGCCAAACCCCTGATGAGCTCATTTGA	GAAGCTCGGCGCTGGAAACATCAAG	452	
OY	876	GGGCGCTTGGGACCAAGACACTTTATGAGAGGTG	TAAAGGCGAGTACAGGGCACTTACAG	935	
Db	453	GGGCGCTTGGGACCAAGACACTTCCAGAGCA	ACCTTGCAGGTGTCAATCCCATCTACAC	512	
OY	936	GCCACCCCAATCTTCAACCGTCTTACATCA	GTGCGCATCTAAGAGTTCCAAACAGCAATGT	995	
Db	513	ACCTCCCTTCTTCTCCGTCTACGTACAGTGC	CGCATCCAGAAATTCACACGCAACGTG	572	
OY	996	ATCCAGGTGGACCAATCTTGGGCTCTTTCG	CGCTCTCGGGATTACTACTTAAACGA	ACT	1055
Db	573	ATCCAAAGTGAACCACTCTTGGCTTGGCTT	TAACCTTCAAGAGTATTATCTCGTGA	CAAAAC	632
OY	1056	GCCAAATGAAAGTCTCACTGCTCTATCTGA	TTTACATGAGAGACTGGGGATGCTGCTG	1115	
Db	633	GAGATGAGAAAGTGTCTACGGGATACCTGA	ACTTATGTCTCAGCTTGGGAAAGTGTGCTG	692	
OY	1116	GGTGGGCGGCCC--ACCTCCA	CGAGGAGCAGATGACAGAGTCTGAGTTGGAGTA	1172	
Db	693	GGAGGAGGGGCGGAGACACCATTCGGG	CCCCAGATGACAGATCTTGACTTTGAGACG	752	
OY	1173	CAGCTGGCCCAACATCACTACAGTGTCC	CAAGACAGCGGCGCAACGAGAGAAAGTCTTACAC	1233	
Db	753	GCGCTGGCCCAACATCACTACCATCC	CCAGAGAAAGCCCGGACGAGAACTCATCTTACAC	812	
OY	1233	AAGATGACCATTTGGAGCTGCAAGGCT	CTGAGGCGCTCATGAGTCTGAGTTCGCTT	1292	
Db	813	AAAGTGAAGGCGGCTGAGTTTGACACTT	GGCGCCGCACTACCTTGGCTTGCCTTCTC	872	
OY	1293	TCTTCTTCTGTCAACCAATGAGTTGAGT	GACTCTGAGCCTGTGGTGTATGGAGT	1352	
Db	873	AAACCAATCTTCTAACCGGTGAGATCA	TAGATCAGAGCGTATGTCTATCGACAA	932	
OY	1353	GATTATTTGACAGCAGGTGTCAAGCT	CTATCAACGCGACGAAACAGCATCCTGA	CAAT	1412
Db	933	GAATTACCTGAGCAAGGTCTCCACCT	CTCATCAACAGACAGCAAAATGTCTGTGA	CAAC	992
OY	1413	TACCGATCTGGAACCTGTGTGA	AAAGCAACCTCAAGCTGAGACCGAGCTTG	AGCT	1472
Db	993	TACATGATCTGGAACTGTATACG	AGAACAGACTCTTCTCTGATCAAGCTT	CCAGAC	1052
OY	1473	GCACAAGAAAGCTGTGAGACCTCTAT	TGGCACTAAGAAAGCTCTGTGTCCG	AGGTGG	1532
Db	1053	GCCACGAGAAAGTTCAATGAAAGTAT	GTATGTGGACCAAGAAAGCTGTCTTCC	CGCTGG	1112
OY	1533	CAGACTGCACTCTCAACACGAGTAC	GCCTTGGCTTCTTGGGATCCCTCTT	CGTG	1592
Db	1113	AAAGTTTGTGAGTGAATACAGAG	AAACCTTGGGCTTCTGCGCCCATGTT	CGTC	1172
OY	1593	AAAGCGACGTTTGAACCGCA	AAAGCAAAATTTGACAGGGGATGATC	AGAGAAATCCGG	1652
Db	1173	AAAGGACCTTCTGAGAGACG	CAAGAAACATAGCAACGAGATCATCTG	AGATTCAG	1232
OY	1653	ACCGCATTTGAGAGGAGCGTGG	GAACAGCTGTGTTTGAATGAGTAA	ACCGCCAGCA	1712
Db	1233	AAAGGCTTTGAAGAGCGCTG	AGCAACCTGTAAGTGAAGATCTCTG	GAATACG	1292
OY	1713	GCAAAGGAAGACAGATGCAT	TATGATGATTGGTTTCCAGACTTAT	TCTGAG	1772

Db	1293	GCAGAGAAAAAGCGGACCGCATATCAACATGATAGGCTAACCCCACTTTATCATGAGAC	1352
Qy	1773	CCCAAGAGCTGATGATGTTTATGACGGGTACGAAATTTCTGAAAGATTCCTTTCCTTCCAA	1832
Db	1353	CCCAAGAGGCTGGCAAAAGTGTTCATATGACTACACCGCTGACGACCTCTACTTTCGAG	1412
Qy	1833	AACATGTTGAATTTGTACAACTTCTCTGCGCAAGGTTATGCTGACCGAGCTCCGAGACCT	1892
Db	1413	AACCCCATTCGGGTTTTTCAACTTCTCTGAGGGGTCACTCCGACCGAGCTCCGAAAGCG	1472
Qy	1893	CCGAGCGGAGACGATGAGACATGACCCCGACAGCACTGATGATGCTCTACTCTTCCAACT	1952
Db	1473	CCCAACAGAGATTCATGTGAGCATGACCCCGCCCATGAGTGAACGCTTACTCTGCGCCAAC	1532
Qy	1953	AAGATGAGATTCGTCTTCCCGCTGGCATCTCGAGGCCCCCTTCTATAGCCCGCAACAC	2012
Db	1533	AAGAACAGAGATTCGTGTTTCCGGCCGGAAATCCTGAGCGGCATTTCTACACCGCTCTTCA	1592
Qy	2013	CCCAAGGCGCTGAACCTTCGGTGGCATCGGTGTGTGTCACTGAGGCAATGATGAGCATGCC	2072
Db	1593	CCCAATCTCTTAAACTTCGCGCGGCATCGGGGTGTCGTCTGGGCGCACGAGCTGACTCATGCT	1652
Qy	2073	TTTATATACCAAGGCGCGAGTATGACAAAGAGGGAACCTGGGCGCCCTGAGTGGCAAT	2132
Db	1653	TTTATATATCAAGGCGCGAGAGTACGACAAAGATGAGGAACCTCGGCGCTGTGTGAGAAAC	1712
Qy	2133	GAGTCCCTGCGAGCTTCCGGAACCAACCGGCGCTGATGAGGAAACGTAACTCATATAC	2192
Db	1713	TCTGTCGTGAGAGGGGTTCAAGCAGCAGACCGCGTGCATGTGTGAGAGCATAGCGCAACTAT	1772
Qy	2193	CAGGTCAATGAGGAGAGAGGCTCAACCGCGCGCAACGCTGAGGAGAACTTGTCTGACAC	2252
Db	1773	AGCGTGAACCGGGAGCGCGGTGAACCGCGCGCACACCTCGCGCGAAACATCGCGCGACAC	1832
Qy	2253	GGGGGCGCTGAAGCGTGCCTCAATGCTTACAAAGCAATGCTGAGAAACATGAGGAGAGAG	2312
Db	1833	GGGGGCGCTCAAGGCGGCGCTATCGGGCGCTTACAGAACTGAGGTCAAGAAAGATGGGGCTGAG	1892
Qy	2313	CAGGAACCTGCGAGCGGTGGGAGCTCAACCAACCAAGCTCTTCTTCGTGGGATTTGACCGAG	2372
Db	1893	CAGACATCTGCCCACTCGGAGTCTACCAACCAACAGCTCTTCTTCTCGAGTTTGGCAGAG	1952
Qy	2373	GTCGTGATGCTTCGATCGCGCACACCAAGAGGCTTCAACGAGGGGCTGTGTGACCGAAC	2432
Db	1953	GTCGTGATGCTTCGATCGCGCACACCCCGAGAGATTCCGACAGAAAGTCTCATCACCGATCCCGAC	2012
Qy	2433	AGCCCTTCGCGCTTCCGCGGTGATCTGAGTCTTCCCAACTTCCCGTACTTCTCGCGGAC	2492
Db	2013	AGCCCTTCGCGCTTCCGCGGTGATCTGAGTCTTCCCAACTTCCCAAGAGTCTCGGAACAC	2072
Qy	2493	TTGCGGCTGCGCTGCGGCTCCCGCATGACCCAGGGGAGCGAGTGTGTGAGGTGTGTGT	2547
Db	2073	TTTCCATGCGCGCGCGGCTCAACCATGAAACCCGCGATCACAAGTGTGAAGTGTGTGT	2127
RESULT 8			
US-08-289-112-1			
Sequence 1, Application US/08289112			
Patent No. 568640			
GENERAL INFORMATION:			
APPLICANT: Yanagisawa, Masashi			
TITLE OF INVENTION: Endothelin Converting Enzyme-1: A			
TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESSER: Arnold, White & Durkee			
STREET: P.O. Box 4433			
CITY: Houston			
STATE: TX			
COUNTRY: USA			
ZIP: 77210-4433			







1094 GGAAGTTTCCGAGGACACAGAAACAACTGGGCTTTGGGTTGGCCCATGTTT 1153  
1591 TGAAGGCCAGTTTGAACCGGCAAGCAAGAAATTTGAGAGGGAGTATGACGAAATCC 1650  
1154 TCAAGACACCTTCGCGGAGACAGCAAGACATAGCCACGAGATCATCTCGAGATTA 1213  
1651 GGAACCGCTTTGAGAGAGCCCTTGAGACAGTGGTTTGGATGATGAGAACCCCGCAG 1710  
1214 AGAAGGATTTGAGAGAAAGCTTAGACCTTGAAAGTGAATGAGAGAAACCCGAAAT 1273  
1711 CAGCCAGAGAAAGACAGATGACATATGATATGATGATGTTTCCAGACTTTATCTG 1770  
1274 CAGCCAGAGAAAGAGCCGATGATCATCAACATGATGATGATGATGATGATGATG 1333  
1771 AGCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1830  
1334 ATCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1393  
1831 AAAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1890  
1394 AAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1453  
1891 CTCCAGCCGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1950  
1454 CCCCCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1513  
1951 CTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2010  
1514 CCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1573  
2011 ACCCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2070  
1574 CACCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1633  
2071 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2130  
1634 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1693  
2131 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2190  
1694 ACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1753  
2191 ACCAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2250  
1754 ACAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1813  
2251 ACCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2310  
1814 ACCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1873  
2311 AGCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2370  
1874 AGCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1933  
2371 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2430  
1934 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1993  
2431 ACAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2490  
1994 ACAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2053  
2491 ACTTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2548  
2054 ACTTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2111

RESULT 10  
US-08-646-273-18  
; Sequence 18, Application us/08646273  
; Patent No. 606502  
; GENERAL INFORMATION:

APPLICANT: Kroeger, Burkhard, Seuberg, Harald, Meyer, Thomas, Schmidt,  
; APPLICANT: Martin, Jacob, Elard, Oter, Rainer, Subkowski, Thomas, Hilten, Heinz.  
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kell & Weinlauf  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,273  
; FILING DATE: 16-NOV-1994  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/03706  
; FILING DATE: 11-NOV-1994  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1703 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA for mRNA  
US-08-646-273-18  
Query Match 24.8%; Score 837.8; DB 3; Length 1703;  
Best Local Similarity 69.0%; Pred. No. 1.7e-190;  
Matches 1177; Conservative 0; Mismatches 522; Indels 6; Gaps 2;  
659 TGGGCGTTCGCTGAGACACCTTCAACAGCTCTGGGACCAAAACGAGCCATGAA 718  
1 TGGGCGTTCGCTGAGACACCTTCAACAGCTCTGGGACCAAAACGAGCCATGAA 60  
719 GCACTGCTTGAACACCACTTCAACAGCTCTGGGACCAAAACGAGCCATGAA 778  
61 GCACTGCTTGAACACCACTTCAACAGCTCTGGGACCAAAACGAGCCATGAA 117  
779 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 838  
118 GATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 177  
839 AGACCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 898  
178 GAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 237  
899 TATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958  
238 CAGAGACACCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297  
959 CATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1018  
298 CGTATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 357  
1019 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078  
358 GGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417  
1079 CTATG 1135  
418 ATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477  
1136 GAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195  
478 CCGGCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537  
1196 CAGAGACACCGGCGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1255



QY 1070 GCTCAGTCTATCTGGAATTACATGAGAACTGGGGATGCTGTGGGTGGGGCCAC 1129  
 DB 1083 CTTGGAGCAATACAGGGGTTCATGAGCAGATGCTCAGCCTCTGGGTG-----CAGA 1136  
 QY 1130 CTCACAGAGGAGCAGATGAGCAGAGTGTGAGATTGAGATACAGCTGGCCCAATCAC 1189  
 DB 1137 CGCTGTGGAACAGAAAGGCCCAAGAGATCTGCAAGTGAACAGAGCTGGCCCAATCAC 1196  
 QY 1190 AGTGGCCAG-----GACCAAGGGCCGAGCAGAGAAATCTACCAAGATGAGCAT 1243  
 DB 1197 TGTGTCAAGATATGACCACTACGAGCAGATGTCAGTCTCATGACCAAGGTGACGT 1256  
 QY 1244 TTGGAGCTCAGAGCTGTGGGCGCTTCATGAGCTGAGTCTGATCTTCTTCTTCT 1303  
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 QY 1304 GTACCAATTGAGTGAAGTGAATCTGTGAGCCTGTGGTGTATAGGAATGATTTTGA 1363  
 DB 1314 CTTCCAGAGGAGACTTTCAGAGGAGAGAGTGTGTCTGTGGCCGACAGATACATGCA 1373  
 QY 1364 GCAGGTGTCAAGTCTATCAACGACAGAAACCAAGATCTTGAACATTAATCTGATCTG 1423  
 DB 1374 GCAGGTGTCCAGTCTATCCGCTCCACACCCCAAGGCTCTGACCAACTACCTGTGTG 1433  
 QY 1424 GAACCTGGTCAAAAGCAACTCAGCTGAGCCGACGAGCTTGAAGTCTGACCAAGAA 1483  
 DB 1434 GCGGTGTGTGTGTCTTGAATGACACTGTCTCCGCCCATTCGTGAGGACCTGACGA 1493  
 QY 1484 GCTGCTGGAGACCTCTATGAGCACTAAGAACTCTGTGTGCGGAGTGGAGACCTGAT 1543  
 DB 1494 GCTGGACACAGAGATGAGAGGGACGACGACCAAGAGACTG---GCCGGGTGTGCTT 1550  
 QY 1544 CTCCACACAGATGAGCCCTTGTGCTTGTGGGTGCTCTCTGTGTGAAGCCAGCTT 1603  
 DB 1551 GGGCCAGGCCAATCGCACTTGTGCAAGGCTGTGGGCGCTCTTGTATAGCACTT 1610  
 QY 1604 TGAACCGGCAAAAGAAATTTGACAGAGGGATGATCAGGAAATCCGACCGCATTTGA 1663  
 DB 1611 CTGAGCTGCCAGCAAAAGCCAGGTGACAGCTAGTGAAGAACATCAAGTACATCTGG 1670  
 QY 1664 GAGAGCCCTGGGAGACGTGTGTGTGTGATGATGAGAAAGCCGCGACGACCAAGAA 1723  
 DB 1671 CCAAGCGCTGAGAGAGCTGAGCTGATGAGAGCCGAGACCAAGGCTGCTCGGGCAA 1730  
 QY 1724 AGCAGATGCCATCTATATATGATGTGTTCCTCCAGACTTATCTGTGAGCCCAAGGCT 1783  
 DB 1731 GCTCCAGTACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1790  
 QY 1784 GATGATGTTTATGACGGGTACGAATTTCTGAAGATTTCTTCTTCAAAACATGTTGA 1843  
 DB 1791 GGAAGAGATGATA---GTTTGAAGTCAATGAGAAACCTAATTCAAGAAATCTTTGA 1847  
 QY 1844 TTTGTACAACTTCTCTGCAAGGTTATGCTGACAGCTCCGCAAGCTCCAGCCGAGA 1903  
 DB 1848 CAGATCCGCTTACAGATCAGGCTCTCATGTTAAGAAATTCGAGAGAGGTGACAGTC 1907  
 QY 1904 CCAAGTGAAGATGACCCCTCCAGACAGTGAATGCTTACTTCACTTCACTAAGATGAT 1963  
 DB 1908 CAGGTGTCTCTCCCTCCACAGAGGCTCAATGCTTACTTCACTTCACTAAGAAACCAAT 1967  
 QY 1964 GGTCTTCCGCGTGGATCCGACAGAGCCCTTCTATAGCCGCAACACCCCAAGGCGCT 2023  
 DB 1968 GGTGTCTCCGCGGAGATCTTGAAGCCCACTTGAAGACCTTGAAGCTTCCCAAGTCTT 2027  
 QY 2024 GAACCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2083  
 DB 2028 CAATTAAGGGGAGATCGGACATCATTTGACATGACTGACCAAGCTTACAGCACTG 2087  
 QY 2084 AGGGCGGAGATGATGACAAAGAGGAACTCGGCGCTGTGTGTGAGAAATGATGCTTCC 2143  
 DB 2088 GGGGGGCGAGATATACGCTCAAGGAACTGTGTGATGATGATGATGATGATGATGAT 2147  
 QY 2144 AGCTTCCGGAACACAGGCTGTGATGAGAAACATGATCAATTAACAGGTCAATGG 2203

DB 2148 CCGCTTCTGCGAAAGCGCTGAGTGCATGCTCCGTCTATGACAACTTCACTGTCTACAA 2207  
 QY 2204 GAGAGGCTCAACCGCCGCCAAGCCTGGGGGAGAACTTGTGACACAGGGGGCTGAA 2263  
 DB 2208 CCAAGCGGTGAAACGGGAAACACACGCTTGGGAGAAACATGCAATATGAGGGGCTCA 2267  
 QY 2264 GGTGCTCTCAATGCTTACAAAGCAATGCTGAGAAAGCAATGGGGAGAGACAGCACTGCC 2323  
 DB 2268 GCTGGCTTACAGCCTTATCAGAAATGAGTGTGGGGAGACGGCCCAAGACACCACTTCC 2327  
 QY 2324 AGCGGTGGGCTCACCAACCAACAGCTCTTCTTGTGGGATTTGCGCAGGTGTGTCTC 2383  
 DB 2328 CCGGCTCAAGTACACATGACAGCAAGCTCTTCTTCAATGCTTGTGCGCAAGCTGTGCAT 2387  
 QY 2384 GGTGCGACACACAGAGAGCTCTCAGAGGGGCTGTGTGACCCCAAGCCTTGGCCG 2443  
 DB 2388 CAAGCGCGGTGTGCTCATCTATCTGACAGGTGTGACTGACAAAGCATGCCCTGAGCA 2447  
 QY 2444 CTTCCGCGTGTGGGACCTCTGCAACCTCCGTGACTTCTGCGGCACTTGGGCTGCC 2503  
 DB 2448 CTACAGGGTGTGGGAGTGTGTCCAGTTTGAAGGTTTGGCGGGCTTTTCACTGTGC 2507  
 QY 2504 TGTGCGCTCCCATGAAACCAAGGAGCTGTGTGAGTGTGTGAGACCTTGG 2555  
 DB 2508 CAAGACTCAACCATGAAACCTTGGCCCAAGATGTTCCGTGTGTGAGCTGG 2559

RESULT 12  
 US-09-704-611-4  
 ; Sequence 4, Application US/09704611  
 ; Patent No. 6548284  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JCR Pharmaceuticals Co., Ltd.  
 ; TITLE OF INVENTION: Membrane-Bound Metalloprotease and Soluble Secreted Form Thereof  
 ; FILE REFERENCE: GP30  
 ; CURRENT APPLICATION NUMBER: US/09/704,611  
 ; CURRENT FILING DATE: 2000-11-03  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SEQ ID NO 4  
 ; LENGTH: 2823  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-704-611-4

Query Match 11.5%; Score 387.6; DB 4; Length 2823;  
 Best Local Similarity 52.3%; Pred. No. 7,4e-83;  
 Matches 1116; Conservative 0; Mismatches 949; Indels 69; Gaps 9;

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 DB 430 CATCTCACACACCCCAAGCTGTGTATGACAGTGTGCAAAATCTGAAACATGAGCA 489  
 QY 587 AGGGGTAGCCCTGTGAGAACTTTTACAGTCTCTGTGGGGCTGTGATTCGAGAA 646  
 DB 490 ATGAGAAACCCCTGTGAATACTTTACAGTACGCTCGGAGGCTGTGAGGACCA 549  
 QY 647 CCCCCCTGGGATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 706  
 DB 550 CGTGATCCAGAGAACCACTCCCGATACAGCGCTTGTGATCTTCGAGGAGAGAGCTGGA 609  
 QY 707 GGCATACAGAGCACTGTGTAAGAAACCAACCTTCACTCAGAGTGAAGTGAAGTGA 766  
 DB 610 GGTATCTCAGAGGGGTGTGAGGATTCCTCACTTCCAGCATGCG---CCGGCCTGGA 666  
 QY 767 GAAGACACAGCGCTTCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 826  
 DB 667 GAAGGCAAGACATATATGCTCTGTGATGAAACCAAGTGTATGAGAAAGAGATCTC 726  
 QY 827 CAGGCACTGAGAGACCTATGAGAAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871  
 DB 727 TGAAGCCCTGTGAGGCTTATTAATAATGATGAGAGGTGTGCTGTGCAATGATTAATG 786



QY 587 AGGGGTGAGCCCTGTGAGGACTTTTACAGTTCTCTCTGTTGGGGGCTGATTGGAGAA 646  
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QY 647 CCCCCTGCGGATGAGGGGCTTCTGCTGGAACAACCTTCAACAGCCTTGGAGCCAAAACA 706  
DB 619 CGTATCTCCAGAGAACCACTCCCGATACAGCGTCTTTGACATCTGTGGGGAGCAGCTGGA 678  
QY 707 GGGCATATGAGACCTGCTTGAATAACCAACCTTCACTCCAGCAGTGAACCTGAGCA 766  
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QY 827 CCAGCACTGAGAGACTCTATTGAGAGATTGGTGTGG-----AACAT 871  
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DB 1036 GAGAGCAACAACCAACGAGGTACGGAAGGCTTACCCGAGTTCATGACGTGTGGCAC 1095  
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DB 1096 TATGCTTGAAGAAAGCAAGAACTGTCTCAAGAGAGGCGCATGTGTGGAGAGATGCG 1155  
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DB 1576 CATGGAAGG---GCCGTGGGCTCCCTTCACTACACGGGCGCTTCTCCAAAGGACAGACA 1632  
QY 1619 AGAAATTGCAAGGGGATGATCAGCAAAATCCGAGCCGCAATTTGAGAGGCGCTTGGACA 1678

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DB 1693 GCTGAACCTGATGAGACGAGAAATCCAAAGAAAGGCGCCAGAAAGGCGCATGAATATAG 1752  
QY 1739 TGAATGATTGGTTTCCGAGCTTTATCTGTGAGGCC-----AAAGACTGGATGATGT 1792  
DB 1753 GGAACAGATTGGCTACCTGACTTACTTTTGAAGATTAACAATTAACCTGATGAGGA 1812  
QY 1793 TTATGACGGGTACGAAATTTCTGAAGATTTCTTCTCCAAAACATGTTGAATTTGACA 1852  
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QY 1853 CTCTCTGCAAGGTTATGCTGACCAAGCTCCGCAAGCTCCACGCGGAGACAGTGGAG 1912  
DB 1873 GAACAATGCCCAGAGAGGCTCAAGAAAGCTTGGGAAAGTGAACGAATCTTGAT 1932  
QY 1913 CATGACCCCCAGACAGTGAATGCTACTACCTTCCAACTAAGAAATGAGATGCTTCC 1972  
DB 1933 CATGGGGCTGCAATGTCTAATGCAATTTCTATCTCCAAACAGAAACAGATGTCTTCC 1992  
QY 1973 CGCTGCAATCTTGCAGGCCCTTCTATGCTCCGCAACCAACCCAGGCCCTGAATCTGG 2032  
DB 1993 AGCAGGATTTCTCAGCGCCCTTCTTCAAGCAAGACCAACACAGTCTTGAATTTGG 2052  
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DB 2053 GGGCATCGGATGTGATGTGGGACAGAGATCAACAGCCTTGTGATGATTAATGTGTGA 2112  
QY 2093 GTATGACAAAGAGGAACTGTGGGCCCTGTGGGAGAAATGATGCTTGGAGCCTTCCG 2152  
DB 2113 CTTTGACAAAGAACGGAACATGTGAGCTGTGTGAGTAACTTCTGGCCCGGACATTTCA 2172  
QY 2153 GAACCAACGCGCTGTGAGAGAAACATGATCAATCAATAAC-----CAGTCAATG 2203  
DB 2173 ACAGAGTGCAGATGATGATGATCATACGCAACCTTCTTGGGAATGACAGACA 2232  
QY 2204 GGAAGAGCTCAACGCGCCGACAGCTGGGGGAGAAATTTGTGACAAACGGGGGCTGAA 2263  
DB 2233 CGAATGTGAACGGAATTCATGCTTCCGGGAGAACTTTGCGCACAGAGGTGTGG 2292  
QY 2264 GGTGCTCAATGCTTACAAAGCATGCTGAGAAAGCATGGGAGAGAGACAGCACTGCC 2323  
DB 2293 ACAGGATACAGGCTTACTACGTGTGCTGTGATGCGGCAAGATCAAGCACTGCC 2352  
QY 2324 AGCCGTGGGGCTCAACCAACCAACGCTCTTCTGTGTGAGATTTGCGAGGTGTGCTC 2383  
DB 2353 GGAATGAACTGACCTATGACCAGCTTTCTTCACTCACTATGCCCAGGTGTGTGG 2412  
QY 2384 GGTCCGCAACACAGAGAGCTCTCAAGAGGGGCTGTGACCGAACCCCAAGCCCTGCCG 2443  
DB 2413 GTCTCTAAGCCGAGTGTGCGGTCCAGTCAATCAAGAGGAGTCAACAGTCTCTTTAA 2472  
QY 2444 CTTCCGCGTGTGGGCACTCTTCCAACTCCGATGCTTCTGCGGCACTTGTGGCTGCC 2503  
DB 2473 GTACAGGTGTGTGGCTTCACTACAGAACTTGCAGGCTTCTGTAGGCAATTCACCTGCC 2532  
QY 2504 TGTGCGCTCCCGCATGAACCCAGGAGCTGTGTGAGGTGTGATCACTGTATCGAGG 2563  
DB 2533 ACAGGACAGCCCATCAACCCATGAAGGAGATGTGCATCTGTATCCAAAGGCTGAGCTA 2592  
QY 2564 AGAAATGCCAGTGTCAACCAAGCTGTGGGCGAGC 2597  
DB 2593 TGTGCGGCCCAAGCCCGCAACCCAGAGGTGCG 2626

RESULT 14  
US-08-646-273-13  
; Sequence 13, Application us/08646273  
; Patent No. 606502  
; GENERAL INFORMATION:





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2004, 10:18:00 ; Search time 1212 Seconds  
(without alignments)  
11836.770 Million cell updates/sec

Title: US-10-681-222-1  
Perfect score: 3377  
Sequence: 1 tcgcggcgccgctgctgcgc.....aaaaaaaaaaaaaaaa 3377

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3377	100.0	3377	7	ABX13166
2	2958.2	87.6	3000	3	AA08402 Human CDN
3	2461.2	72.9	2602	2	AA234326 Human neu
4	2461.2	72.9	2602	3	AACT8592 Human PRO
5	2461.2	72.9	2602	4	AA546134 Human DNA
6	2461.2	72.9	2602	4	ABX78737 Human PRO
7	2461.2	72.9	2602	7	ACA75709 Human hum
8	2461.2	72.9	2602	7	ACA71189 Human sec
9	2461.2	72.9	2602	7	ACC87717 Human sec
10	2461.2	72.9	2602	7	ACC87103 Human sec
11	2461.2	72.9	2602	7	ACD04276 Human sec
12	2461.2	72.9	2602	7	ACA69607 Human sec
13	2461.2	72.9	2602	7	ACA90452 Human enco
14	2461.2	72.9	2602	7	ACC89559 Human hum
15	2461.2	72.9	2602	7	ACA9350 Human sec
16	2461.2	72.9	2602	7	ACA93992 Human hum
17	2461.2	72.9	2602	7	ACD15385 Human sec
18	2461.2	72.9	2602	7	ACD08972 Human sec
19	2461.2	72.9	2602	7	ACF19704 Human sec
20	2461.2	72.9	2602	7	ACF15613 Human sec
21	2461.2	72.9	2602	7	ACD42859 Human hum
22	2461.2	72.9	2602	7	ACA72980 Human PRO
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24	2461.2	72.9	2602	7	ACD01967	ACD01967 Novel hum
25	2461.2	72.9	2602	7	ACA92159	ACA92159 Novel hum
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27	2461.2	72.9	2602	7	ACA89584	ACA89584 CDNA enco
28	2461.2	72.9	2602	7	ACA73594	ACA73594 Human sec
29	2461.2	72.9	2602	7	ACA05909	ACA05909 Human sec
30	2461.2	72.9	2602	7	ACA66743	ACA66743 CDNA enco
31	2461.2	72.9	2602	7	ACF20318	ACF20318 Human sec
32	2461.2	72.9	2602	7	ACF19704	ACF19704 Human sec
33	2461.2	72.9	2602	7	ACD11992	ACD11992 Human sec
34	2461.2	72.9	2602	7	ACF13157	ACF13157 Human sec
35	2461.2	72.9	2602	7	ACD25260	ACD25260 Human sec
36	2461.2	72.9	2602	7	ACF00309	ACF00309 Human sec
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41	2461.2	72.9	2602	7	ACA88792	ACA88792 Human hum
42	2461.2	72.9	2602	7	ACA70234	ACA70234 Human sec
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44	2461.2	72.9	2602	7	ACF74371	ACF74371 Human sec
45	2461.2	72.9	2602	7	ACD15999	ACD15999 Human sec

## ALIGNMENTS

RESULT 1	ABX13166	standard; CDNA; 3377 BP.
XX	ABX13166	
XX	AC	ABX13166;
XX	12-MAY-2003	(first entry)
XX	Human CDNA encoding a zinc metalloprotease.	
XX	Human, ss; gene; zinc metalloprotease; metastatic cancer; tumour;	
KW	osteoarthritis; rheumatoid arthritis; septic arthritis;	
KW	periodontal disease; corneal ulceration; proteinuria;	
KW	coronary thrombosis; aneurysm aortic disease; birth control;	
KW	dystrophic epidermolysis bullosa; degenerative cartilage loss;	
KW	inflammatory response; osteopenia; tempo mandibular joint disease;	
KW	nervous system demyelinating disease; chromosome 3.	
XX	OS	Homo sapiens.
XX	XX	
XX	Key	Location/Qualifiers
FT	FT	114..2549
FT	FT	CD5
FT	FT	/*tag= a "Zinc metalloprotease"
FT	FT	/note= "this CDS (minus the stop codon) is specifically
FT	FT	claimed in claim 10"
PN	US6482629-B1.	
XX	19-NOV-2002.	
XX	23-MAR-2001; 2001US-00819989.	
XX	29-MAR-2001; 2001US-00819989.	
XX	(APPL-) APPLERA CORP.	
XX	Wei M, Yan C, Di Francesco V, Beasley EM;	
XX	WPI; 2003-298138/29.	
XX	P-FSDB; ABG76487.	
XX	DR	New human zinc metalloprotease enzymes and nucleic acids encoding them,
XX	PT	useful as models in developing and identifying human therapeutics, or as
XX	PT	targets for developing therapeutic agents that modulate enzyme activity.

PS Claim 1; Fig 1; 49pp; English.

The invention relates an isolated nucleic acid molecule (cDNA and gene) comprising a sequence encoding a human zinc metalloproteinase. Also included are vectors and host cells for expression of the polypeptide. The human zinc metalloproteinase and nucleic acids encoding them are useful as models in the development of human therapeutics, in the identification of therapeutic proteins, as targets for the development of human therapeutic agents that modulate enzyme activity in cells and tissues expressing the enzyme, and as query sequences for sequence database searches for the identification of other family members or related sequences. The proteins may further be used to raise antibodies or to elicit another immune response, as a reagent in assays to quantitatively determine protein levels in biologic fluids, as markers for tissues in which the corresponding protein is expressed, as a target for diagnosing a disease or predisposition to a disease-mediated by the peptide, and for treating a disorder characterised by an absence or unwanted expression of the protein (e.g. metastatic cancer, tumour, osteoarthritis, rheumatoid arthritis, septic arthritis, periodontal disease, corneal ulceration, proteinuria, coronary thrombosis, aneurysm aortic disease, dystrophic epidermolysis bullosa, degenerative cartilage loss, inflammatory response, osteopenia, temporo mandibular joint disease and nervous system demyelinating disease). The protein is also of use in birth control. The nucleic acids are useful as probes and primers, for constructing recombinant vectors, for monitoring effectiveness of modulating compounds on the expression or activity of the enzyme gene in clinical trials, and for constructing recombinant vectors. The gene for the metalloproteinase is located on chromosome 3. The present sequence is a cDNA encoding the human zinc metalloproteinase.

Sequence 3377 BP; 747 A; 973 C; 982 G; 675 T; 0 U; 0 Other;

Query Match	100.0%;	Score 3377;	DB 7;	Length 3377;
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Best Local Similarity: 100.00%, Freq. NO: 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGGAGCGGGGCCAGCTGCCGGGAGCCCTGAATTCACCGCTGGCCGACCTCCACCATGAACG	120
Db	61	GGGAGCGGGGCCAGCTGCCGGGAGCCCTGAATTCACCGCTGGCCGACCTCCACCATGAACG	120
QY	121	TCGGAGTGCAGAGAGCTGGGAGCTGGGACAGCAATGATGAGATACAAACGGGCGACGCTTC	180
Db	121	TCGGAGTGCAGAGAGCTGGGAGCTGGGACAGCAATGATGAGATACAAACGGGCGACGCTTC	180
QY	181	GGAGTGAAGAAGCACCCCGAGACCCCGCTGAGAGGGCGGGGCGCTCCCGGACGCCATGAGAG	240
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Db	241	TGGGCAAGGGGGGCTTCCCTTTTCTACCAAGGCCCAAGCTCTGGCATGACGCTTGACAC	300
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QY	361	TCTGCTCTAGGACTATGATGGTGGGATTTCCAGAAAGGGGACAAAGACAGCTGTTAGGCTCACGCA	420
Db	361	TCTGCTCTAGGACTATGATGGTGGGATTTCCAGAAAGGGGACAAAGACAGCTGTTAGGCTCACGCA	420
QY	421	CGAGACTGGAGCTGGTCTTTAGCGAGGTGCTCTCTACTGCTGGCTGCACTGCTTTGGGCT	480
Db	421	CGAGACTGGAGCTGGTCTTTAGCGAGGTGCTCTCTACTGCTGGCTGCACTGCTTTGGGCT	480
QY	481	GCCATTGAGCCCTTAGGGGCTCCAGTACCAACAAGAGCCCATCCACAAGACACTGGCTTTAG	540
Db	481	GCCATTGAGCCCTTAGGGGCTCCAGTACCAACAAGAGCCCATCCACAAGACACTGGCTTTAG	540
QY	541	AGGCTTGATTCGAGTGGCTGGAAAAATCTCGAGAGTCCCTGGACCGAAGGGGTGAGCCCT	600

Db	541	AGGCTGCGATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCT	600
Oy	601	GTGAGGACTTTTACCACTTCTCTGTGGGGGCTGGATTGGAGGAAACCCCTGCGGATG	660
Db	601	GTGAGGACTTTTACCACTTCTCTGTGGGGGCTGGATTGGAGGAAACCCCTGCGGATG	660
Oy	661	GGGCTTCGCTGGGAACACCTTCAACAGCCCTGGGGACAAAAACAGGCCATATCTGAAGC	720
Db	661	GGGCTTCGCTGGGAACACCTTCAACAGCCCTGGGGACAAAAACAGGCCATATCTGAAGC	720
Oy	721	ACCTGCTTGA AAAACCAACCTTCAACTCCAGACGTGAAGCTGAGCAGAGAACAAGCGCT	780
Db	721	ACCTGCTTGA AAAACCAACCTTCAACTCCAGACGTGAAGCTGAGCAGAGAACAAGCGCT	780
Oy	781	TCCTACCTATCTTGGCTTCAAGTGGAGGGCAATTGAGAGCTGGAGGCCCACTGAGAG	840
Db	781	TCCTACCTATCTTGGCTTCAAGTGGAGGGCAATTGAGAGCTGGAGGCCCACTGAGAG	840
Oy	841	ACCTCATTTGAGAAATTTGTGTGTGGAACAATTACGGGGCCCTGGGACCAAGAACATTTTA	900
Db	841	ACCTCATTTGAGAAATTTGTGTGTGGAACAATTACGGGGCCCTGGGACCAAGAACATTTTA	900
Oy	901	TGAGGTGTGTAAGAGCACTAGACGGGACCTTACAGGGCCACCCCATTTCTTACCGTCTACA	960
Db	901	TGAGGTGTGTAAGAGCACTAGACGGGACCTTACAGGGCCACCCCATTTCTTACCGTCTACA	960
Oy	961	TCAGTGGCCGACTCTAAGATTCCAAACAGCAATGTATTCAGAGTGGACCAAGCTGGGCTCT	1020
Db	961	TCAGTGGCCGACTCTAAGATTCCAAACAGCAATGTATTCAGAGTGGACCAAGCTGGGCTCT	1020
Oy	1021	TTCTGCCCCCTCGGGATTTACTTATAACAGAACTGGCAATGAAAGTGTCACTGCGCT	1080
Db	1021	TTCTGCCCCCTCGGGATTTACTTATAACAGAACTGGCAATGAAAGTGTCACTGCGCT	1080
Oy	1081	ATCTGAAATTACAATGGAAGAACTGGGGATGCTGCTGGGTGGGGCGGCCCACTCCACGAGGG	1140
Db	1081	ATCTGAAATTACAATGGAAGAACTGGGGATGCTGCTGGGTGGGGCGGCCCACTCCACGAGGG	1140
Oy	1141	AGCAGATGTCAGACAGTCTCTGAGTTTGAGATATACAGCTGGGCCCAATCACAGTGGCCGAGG	1200
Db	1141	AGCAGATGTCAGACAGTCTCTGAGTTTGAGATATACAGCTGGGCCCAATCACAGTGGCCGAGG	1200
Oy	1201	ACGACGGCGCGACGAGAGGAAATCTTACCAACAAGATGAGCATTTCCGAGCTGAGGCTC	1260
Db	1201	ACGACGGCGCGAGAGAGGAAATCTTACCAACAAGATGAGCATTTCCGAGCTGAGGCTC	1260
Oy	1261	TGGGCGCCCTCATGGA CTGGCTTGA GTTCTGTCTTCTTGCTGTCAACAATTGGAGTTGA	1320
Db	1261	TGGGCGCCCTCATGGA CTGGCTTGA GTTCTGTCTTCTTGCTGTCAACAATTGGAGTTGA	1320
Oy	1321	GTGACTCTGAGCCCTGTGTGTGTATGAGGATGTGATTTTGGACAGAGTGTCAAGACTCA	1380
Db	1321	GTGACTCTGAGCCCTGTGTGTGTATGAGGATGTGATTTTGGACAGAGTGTCAAGACTCA	1380
Oy	1381	TCACACCCGACGGAACCAAGCATCTCTGAAACAATTACCTGATCTGGAACTGTGTCAAAAGA	1440
Db	1381	TCACACCCGACGGAACCAAGCATCTCTGAAACAATTACCTGATCTGGAACTGTGTCAAAAGA	1440
Oy	1441	CAACCTCAAGCCTGGAACCGACGCTTTTGA GTCTGCAACAAGAAAGCTGTGGAGCCCTCT	1500
Db	1441	CAACCTCAAGCCTGGAACCGACGCTTTTGA GTCTGCAACAAGAAAGCTGTGGAGCCCTCT	1500
Oy	1501	ATGGCACTAAGAACTCTGTGTGTGTCGAGGTGGAGACTTGATTTCCAAACGAGTAAAG	1560
Db	1501	ATGGCACTAAGAACTCTGTGTGTGTCGAGGTGGAGACTTGATTTCCAAACGAGTAAAG	1560
Oy	1561	CCCTTGGCTTTGCTTGGGGGCTCCTCTTGTGAAAGGCAAGTTTGAACGGCAAAAGCAAG	1620
Db	1561	CCCTTGGCTTTGCTTGGGGGCTCCTCTTGTGAAAGGCAAGTTTGAACGGCAAAAGCAAG	1620
Oy	1621	AAATTTGACAGAGGAGTATCAAGCAAAATCCGGAACCGCATTTGAGAGGCTCTGGGACAGC	1680

Db 1621 AATTCAGAGGAGATGATCAGCGAATCCGACCCGATTTGAGAGGCGCTGGGACAGC 1680  
Qy 1681 TGGTTGAGATGATGAGAAACCCCGCAGGCGAGCGAAGGAAAGAGATGCCATCTATG 1740  
Db 1681 TGGTTGAGATGAGAAACCCCGCAGGCGAGCGAAGGAAAGAGATGCCATCTATG 1740  
Qy 1741 ATATGATGATTTCCAGACTTTATCTTGAGGCCCAAGAGCTGATGATGTTATGACG 1800  
Db 1741 ATATGATGATTTCCAGACTTTATCTTGAGGCCCAAGAGCTGATGATGTTATGACG 1800  
Qy 1801 GGTACGAAATTTCTGAAGATTTCTTCTCCAAAATGTTGAAATTTGTACAACTTCTG 1860  
Db 1801 GGTACGAAATTTCTGAAGATTTCTTCTCCAAAATGTTGAAATTTGTACAACTTCTG 1860  
Qy 1861 CCAAGGTTATGCTGACACACTCCGCAAGCTCCGACCGAGACCAATGAGATGACCC 1920  
Db 1861 CCAAGGTTATGCTGACACACTCCGCAAGCTCCGACCGAGACCAATGAGATGACCC 1920  
Qy 1921 CCCAGACAGTAAATGCTTACCTTCACTAAGATGATGCTTCCCGCTGGCA 1980  
Db 1921 CCCAGACAGTAAATGCTTACCTTCACTAAGATGATGCTTCCCGCTGGCA 1980  
Qy 1981 TCCGAGAGCCCTCTTATGACCCGCAACCAAGCCCAAGGCTGAACTTGATGCTG 2040  
Db 1981 TCCGAGAGCCCTCTTATGACCCGCAACCAAGCCCAAGGCTGAACTTGATGCTG 2040  
Qy 2041 GTGTGCTCATGAGGCTGATGATGATGCTTGTATGACCAAGGCGGAGATATACA 2100  
Db 2041 GTGTGCTCATGAGGCTGATGATGATGCTTGTATGACCAAGGCGGAGATATACA 2100  
Qy 2101 AAGAAAGGAACTGCGGCGCTGGTGGCAGATGATGCTTGGAGCGCTTCGCGAACACA 2160  
Db 2101 AAGAAAGGAACTGCGGCGCTGGTGGCAGATGATGCTTGGAGCGCTTCGCGAACACA 2160  
Qy 2161 CGGCTGCTGATGAGAAACAGTACATCATATACAGGTCAATGGGAGAGGCTCAACGCGC 2220  
Db 2161 CGGCTGCTGATGAGAAACAGTACATCATATACAGGTCAATGGGAGAGGCTCAACGCGC 2220  
Qy 2221 GCCAGAGCTGGGGGAGAAATGCTGACAAACGGGGGGCTGAAGGCTGCTTCAATGCTT 2280  
Db 2221 GCCAGAGCTGGGGGAGAAATGCTGACAAACGGGGGGCTGAAGGCTGCTTCAATGCTT 2280  
Qy 2281 ACAAAAGATGCTGAGAAAGATGAGGAGAGAGCACTGCGAGCGCTGGGGCTCACCA 2340  
Db 2281 ACAAAAGATGCTGAGAAAGATGAGGAGAGAGCACTGCGAGCGCTGGGGCTCACCA 2340  
Qy 2341 ACCACAGCTCTTCTGAGGATTTGCGCAGGTGTGTGCTCGATCCGACACCAAGAGA 2400  
Db 2341 ACCACAGCTCTTCTGAGGATTTGCGCAGGTGTGTGCTCGATCCGACACCAAGAGA 2400  
Qy 2401 GCTCTCAAGAGGGGCTGTGTACCGAACCGGCTGCGCTTCCGCTGTGTGGGCA 2460  
Db 2401 GCTCTCAAGAGGGGCTGTGTACCGAACCGGCTGCGCTTCCGCTGTGTGGGCA 2460  
Qy 2461 CTCTCTCAACCTGCGGATCTTCTGAGGAGCACTTGGGCTGCGCTTCCCGCATGA 2520  
Db 2461 CTCTCTCAACCTGCGGATCTTCTGAGGAGCACTTGGGCTGCGCTTCCCGCATGA 2520  
Qy 2521 ACCCAGGAGAGCTGTGTGAGGTGTGTACCTGTGATCAGAGGAGAAATGCCAGCTGTC 2580  
Db 2521 ACCCAGGAGAGCTGTGTGAGGTGTGTACCTGTGATCAGAGGAGAAATGCCAGCTGTC 2580  
Qy 2581 ACCAGACCTGGGGAGCTCTCTGACAAAGCTGTTTGTCTTGGGTTGGAGAGAAAGCAA 2640  
Db 2581 ACCAGACCTGGGGAGCTCTCTGACAAAGCTGTTTGTCTTGGGTTGGAGAGAAAGCAA 2640  
Qy 2641 TGCAGAGCTGGGCTGAGTCTAGTCCCTCCCGCAGAGGTGACATGAGTACAGACCTCTCT 2700  
Db 2641 TGCAGAGCTGGGCTGAGTCTAGTCCCTCCCGCAGAGGTGACATGAGTACAGACCTCTCT 2700  
Qy 2701 CAATCAACCAATGCTGCTTGTGGGGGTGCGCTGCTGACAGAGAGCCCAACA 2760  
Db 2701 CAATCAACCAATGCTGCTTGTGGGGGTGCGCTGCTGACAGAGAGCCCAACA 2760

Qy 2761 TTCACTGTGACATCTTTCCGTGTCACCTGCGCTGAGAGAGGTCTGGGTGGGAGGCGCAGT 2820  
Db 2761 TTCACTGTGACATCTTTCCGTGTCACCTGCGCTGAGAGAGGTCTGGGTGGGAGGCGCAGT 2820  
Qy 2821 TCCCATATGAGAGAGGTCTGCTCTTGTGTCGCCAGGCTCACTAGGCTGGCGGCAATGAGG 2880  
Db 2821 TCCCATATGAGAGAGGTCTGCTCTTGTGTCGCCAGGCTCACTAGGCTGGCGGCAATGAGG 2880  
Qy 2881 GCTGCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 2940  
Db 2881 GCTGCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 2940  
Qy 2941 CCCAGGCTACACTGAGTGGCACTTATGAGGAGTGAAGTCAAGTCTGCTGCTGCTGCTGCTG 3000  
Db 2941 CCCAGGCTACACTGAGTGGCACTTATGAGGAGTGAAGTCAAGTCTGCTGCTGCTGCTGCTG 3000  
Qy 3001 GGGCTACCCGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060  
Db 3001 GGGCTACCCGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060  
Qy 3061 TTCACTGACAGCTCTGATGAGAAAGCCCAAGGCTCTGAAAGCTCTGCTGCTGCTGCTGCT 3120  
Db 3061 TTCACTGACAGCTCTGATGAGAAAGCCCAAGGCTCTGAAAGCTCTGCTGCTGCTGCTGCT 3120  
Qy 3121 TTCCCTGGGCTGAGAGGAGAGAGTATGATGATGAGGAGGAGTTCCTGCTGCTGCTGCTG 3180  
Db 3121 TTCCCTGGGCTGAGAGGAGAGTATGATGATGAGGAGGAGTTCCTGCTGCTGCTGCTGCTG 3180  
Qy 3181 GCACAAAGCTTATGACATATGATTTGATTTCTCCCTGAGCAAAAGAGAGAGAGATGAGAG 3240  
Db 3181 GCACAAAGCTTATGACATATGATTTGATTTCTCCCTGAGCAAAAGAGAGAGAGATGAGAG 3240  
Qy 3241 GGAAGAGAGAGAGAGAGATTTATTTTACAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 3300  
Db 3241 GGAAGAGAGAGAGAGAGATTTATTTTACAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 3300  
Qy 3301 CCTTATGAGAGCCTGAGCAATTAACAGATGATCCGCTCAAAAAA 3360  
Db 3301 CCTTATGAGAGCCTGAGCAATTAACAGATGATCCGCTCAAAAAA 3360  
Qy 3361 AAAAAAAAAAAAAAAAAA 3377  
Db 3361 AAAAAAAAAAAAAAAAAA 3377

RESULT 2  
AAA08402  
ID AAA08402 standard; cDNA; 3000 BP.  
XX  
AC AAA08402;  
XX  
DT 13-JUL-2000 (first entry)  
XX  
XX  
DE Human neurotransmitter associated nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; neurotransmitter; diagnosis; antiparkinsonian; neuroleptic;  
KW anticonvulsant; nootropic; tranquilizer; neuroprotective; cytoskeletal;  
KW antidepressant; antidiabetic; gynecological; immunosuppressive;  
KW neurological disorder; hormone-related disease; Parkinson's disease;  
KW schizophrenia; epilepsy; female reproductive disorder;  
KW attention deficit disorder; ss.  
OS Homo sapiens.  
XX  
XX  
PN MO200012685-A2.  
XX  
PD 09-MAR-2000.  
XX  
XX  
PF 26-AUG-1999; 99MO-US019615.  
XX  
XX 01-SEP-1998; 98US-00144952.  
PR 01-SEP-1998; 98US-0155194P.

XX (INCY-) INCYTE PHARM INC.  
PA Walker MG, Volkmutz W, Klingler TM;  
PI WPI; 2000-375619/32.  
XX  
PT A new purified polynucleotide comprising a gene that is coexpressed with  
PT neurotransmitter-processing-specific genes in biological samples for  
PT diagnosing, treating or preventing neurological and hormone-related  
PT diseases.  
PS  
PS Claim 2; Page 32-33; 36pp; English.  
XX  
XX The present invention describes a purified polynucleotide comprising a  
CC gene that is coexpressed with one or more neurotransmitter-processing-  
CC specific genes in biological samples. The neurotransmitter-processing-  
CC specific genes are L-tyrosine hydroxylase (TH), aromatic amino acid  
CC decarboxylase (AADC), dopamine beta-hydroxylase (DBH), nicotinic  
CC acetylcholine receptor alpha3 subunit precursor (nAChR-alpha3),  
CC acetylcholinesterase (AChE), human cocaine and amphetamine regulated  
CC transthyretin (hTTR), vesicular monoamine transporter 1 (VMAT1), and ARX  
CC homodomain protein. The present sequence represents a neurotransmitter  
CC associated nucleotide sequence from the present invention. The  
CC polynucleotides from the present invention can have antiparkinsonian,  
CC neuroleptic, anticonvulsant, nootropic, tranquilizer, neuroprotective,  
CC cyostatic, antidepressant, antidiabetic, gynecological and  
CC immunosuppressive activities. They can be used for diagnosing, treating,  
CC preventing or evaluating therapies for neurological and hormone-related  
CC diseases, particularly Parkinson's disease, schizophrenia, epilepsy,  
CC female reproductive disorders and attention deficit disorder. The gene  
CC products are therapeutic proteins and targets of therapeutics against the  
CC diseases  
CC  
SQ Sequence 3000 BP; 672 A; 845 C; 858 G; 625 T; 0 U; 0 Other;  
Query Match 87.6%; Score 2958.2; DB 3; Length 3000;  
Best local Similarity .99.4%; Pred. No. 0;  
Matches 2980; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
QY 360 CTCTGCTCTAGAGATATGTTGGATTCAGAGGGGACAAAGAGCTGTAGGCTCAGC 419  
DB 2 CTGGAGACTGAGCAAGCTGGGATTCAGAGGGGACAAAGAGCTGTAGGCTCAGC 61  
QY 420 ACCGAGCTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 479  
DB 62 ACCGAGCTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 121  
QY 480 TGCTTGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 539  
DB 122 TGCTTGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 181  
QY 540 GAGGCTGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 599  
DB 182 GAGGCTGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 241  
QY 600 TGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 659  
DB 242 TGTGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 301  
QY 660 GGGGCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 719  
DB 302 GGGGCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 361  
QY 720 CACTGTGTTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 779  
DB 362 CACTGTGTTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 421  
QY 780 TTCTACTATCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 839  
DB 422 TTCTACTATCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 481  
QY 840 GACCTATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 899

DB 482 GACCTATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 541  
QY 900 ATGAGAGCTGTAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 959  
DB 542 ATGAGAGCTGTAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 601  
QY 960 ATGAGAGCTGTAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1019  
DB 602 ATGAGAGCTGTAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 661  
QY 1020 TTTCTGCTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1079  
DB 662 TTTCTGCTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 721  
QY 1080 TATCTGAGATTAATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1139  
DB 722 TATCTGAGATTAATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 781  
QY 1140 GAGCAGATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1199  
DB 782 GAGCAGATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 841  
QY 1200 GACAGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1259  
DB 842 GACAGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 901  
QY 1260 CTGGGCTCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1319  
DB 902 CTGGGCTCTTCTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 961  
QY 1320 AGTGAATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1379  
DB 962 AGTGAATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1021  
QY 1380 ATCAACCGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1439  
DB 1022 ATCAACCGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1081  
QY 1440 ACAACCTCAAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1499  
DB 1082 ACAACCTCAAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1141  
QY 1500 TATGAGACTTAAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1559  
DB 1142 TATGAGACTTAAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1201  
QY 1560 GCCCTTGGCTTGTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1619  
DB 1202 GCCCTTGGCTTGTGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1261  
QY 1620 GAAATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1679  
DB 1262 GAAATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1321  
QY 1680 CTGGTGTGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1739  
DB 1322 CTGGTGTGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1381  
QY 1740 GATATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1799  
DB 1382 GATATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1441  
QY 1800 GGGTATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1859  
DB 1442 GGGTATGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1501  
QY 1860 GCCAAGTATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1919  
DB 1502 GCCAAGTATGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1561  
QY 1920 CCCAGAGAGAGAGCTGTAGAGAGGCTCTTACTGCTGTGAGAGCTGTAGGCTCAGC 1979





XX	08-APR-1998;	98US-0081070P.
PR	08-APR-1998;	98US-0081071P.
PR	09-APR-1998;	98US-0081195P.
PR	09-APR-1998;	98US-0081203P.
PR	09-APR-1998;	98US-0081229P.
PR	15-APR-1998;	98US-0081817P.
PR	15-APR-1998;	98US-0081838P.
PR	15-APR-1998;	98US-0081952P.
PR	15-APR-1998;	98US-0081955P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082804P.
PR	23-APR-1998;	98US-0082767P.
PR	23-APR-1998;	98US-0082767P.
PR	27-APR-1998;	98US-0083336P.
PR	28-APR-1998;	98US-0083332P.
PR	29-APR-1998;	98US-0083392P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-0083545P.
PR	29-APR-1998;	98US-0083554P.
PR	29-APR-1998;	98US-0083558P.
PR	29-APR-1998;	98US-0083559P.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084441P.
PR	06-MAY-1998;	98US-0084441P.
PR	07-MAY-1998;	98US-0084598P.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085333P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-0085700P.
PR	15-MAY-1998;	98US-0085704P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086352P.
PR	22-MAY-1998;	98US-0086414P.
PR	22-MAY-1998;	98US-0086430P.
PR	22-MAY-1998;	98US-0086466P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
PR	28-MAY-1998;	98US-0087208P.
PR	30-JUL-1998;	98US-0094651P.
PR	11-SEP-1998;	98US-0100038P.
XX	(GETH ) GENENTECH INC.	
XX	PA	
XX	PI	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX	DR	WPI, 1999-551358/46.
XX	DR	P-PSDB; AAAY41774.
XX	PT	New secreted and transmembrane polypeptides and their polynucleotides
XX	PT	useful for treating blood coagulation disorders, cancers and cellular
XX	XX	adhesion disorders.
XX	XX	Claim 2, Fig 224, 530pp; English.
XX	XX	

CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ3391 to AAZ4338, and AA4165 to  
CC AA41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention

XX Sequence 2602 BP; 577 A; 737 C; 767 G; 521 T; 0 U; 0 Other;

SQ Query Match            72.9%; Score 2461.2; DB 2; Length 2602;  
Best Local Similarity    99.5%; Pred. No. 0;  
Matches 2469; Conservative    0; Mismatches    13; Indels    0; Gaps    0;

QY	360	TTCTGCTCTACGACCTAATGCTGGGAATTCAGAAAGGGGACAAACAGCTGTATGGCTCAGC	419
Db	121	CTGGAGCTGGCAGCAACAGTGGGATTCAGAAAGGGGACAAACAGCTGTATGGCTCAGC	180
QY	420	ACGAGCTGAGAGCTGCTTTAAGCAGGTGCTCTCTACTGCTGGCTGACCTGTCTTCTGGGC	479
Db	181	ACGAGCTGAGAGCTGCTTTAAGCAGGTGCTCTCTCTACTGCTGGCTGACCTGTCTTCTGGGC	240
QY	480	TGCTCTGTGGCCCTTAAGGGGTCCACTAACACGAAACCCATCCCAACAGACCTGTGCTTACA	539
Db	241	TGCTCTGTGGCCCTTAAGGGGTCCACTAACGAAACCCATCCCAACAGACCTGTGCTTACA	300
QY	540	GAGGCTGTCATTCGAGTGGCTGGAAGAAAATCCTGAGTCCCTGACCCGAGGGGTAGGCC	599
Db	301	GAGGCTGTCATTCGAGTGGCTGGAAGAAAATCCTGAGTCCCTGACCCGAGGGGTAGGCC	360
QY	600	TGTAGAGACTTTTAAACAGTTCCTCTGTGGGGCTGGAATTCGAGGAACCCCTGCGCAT	659
Db	361	TGTAGAGACTTTTAAACAGTTCCTCTGTGGGGCTGGAATTCGAGGAACCCCTGCGCAT	420
QY	660	GGGGGTTCTGCTGTGGAACACCTTAAACAGCTCTGGGACCAAAACCGAGGCATACTGAAG	719
Db	421	GGGGGTTCTGCTGTGGAACACCTTAAACAGCTCTGGGACCAAAACCGAGGCATACTGAAG	480
QY	720	CACCTGTCTTGAAGAACACCAACCTTCAACTCCAGCAGTGAAGCTGAGCAAGAACACAGGC	779
Db	481	CACCTGTCTTGAAGAACACCAACCTTCAACTCCAGCAGTGAAGCTGAGCAAGAACACAGGC	540
QY	780	TTCTAAGCTATCTTGCTCTACAGGTGAGGCGCATTTAGAGAGCTGGGAGCCCAAGCACTAGA	839
Db	541	TTCTAAGCTATCTTGCTCTACAGGTGAGGCGCATTTAGAGAGCTGGGAGCCCAAGCACTAGA	600
QY	840	GACCTCAATGGAAGATTGTTGGTTTGGAACTTAAACGGGGCCCTGAGAACAGAAACAATTT	899
Db	601	GACCTCAATGGAAGATTGTTGGTTTGGAACTTAAACGGGGCCCTGAGAACAGAAACAATTT	660
QY	900	ATGAGAGTGTGAAGGACAGTACAGGAGCCTTACAGGGCCACCCATTTCTTACCGCTTAC	959
Db	661	ATGAGAGTGTGAAGGACAGTACAGGAGCCTTACAGGGCCACCCATTTCTTACCGCTTAC	720
QY	960	ATCAGTGGCCGACTCTAAGAGTTCCAACAGCAATGTATCCAGGTGGACCAATCTGGGGTC	1019
Db	721	ATCAGTGGCCGACTCTAAGAGTTCCAACAGCAATGTATCCAGGTGGACCAATCTGGGGTC	780
QY	1020	TTTCTGCCCCCTCGGGAAATTACTACTTAAACGAACCTGCATTTGAGAAAGTCTCACTGCC	1079
Db	781	TTTCTGCCCCCTCGGGAAATTACTACTTAAACGAACCTGCATTTGAGAAAGTCTCACTGCC	840
QY	1080	TATCTGATTTACATGAGGAACCTGGGAGTGTGCTGTGGGTGGGCGGCCCACTTCCACGAGG	1139
Db	841	TATCTGATTTACATGAGGAACCTGGGAGTGTGCTGTGGGTGGGCGGCCCACTTCCACGAGG	900
QY	1140	GAGCAGATGACGACAGTGTCTGGAATTTGGAGTTACAGCTGGGCCAATCAACAGTGGCCGAG	1199
Db	901	GAGCAGATGACGACAGTGTCTGGAATTTGGAGTTACAGCTGGGCCAATCAACAGTGGCCGAG	960

QY	1200	TACCAAGCGGCGCCGACGAGAGAAAGATCTAACACAAGATGAGCATTTGCGACTCGAGGCT	1253
Db	961	GACCAAGCGGCGCGACGAGAGAAAGATCTAACACAAGATGAGCATTTGCGACTCGAGGCT	1020
QY	1260	CTGGGCGCCTCCATGGA CTGGCTTGAGTTCCTGCTCTTCTTGCTGCTGACCAATTGGAGTTG	1319
Db	1021	CTGGGCGCCTCCATGGA CTGGCTTGAGTTCCTGCTCTTCTTGCTGCTGACCAATTGGAGTTG	1080
QY	1320	AGTGA CTGTAGCCCTGTGTGTGTGTATGGATGATTA TTTTGACAGAGTGTCAAGGCTC	1379
Db	1081	AGTGA CTGTAGCCCTGTGTGTGTGTATGGATGATTA TTTTGACAGAGTGTCAAGGCTC	1140
QY	1380	ATCAACCGGACGGAA CCAAGCATCTGTAA CAATTACTGATCTGGAA CCTGTGTAAAG	1439
Db	1141	ATCAACCGGACGGAA CCAAGCATCTGTAA CAATTACTGATCTGGAA CCTGTGTAAAG	1200
QY	1440	ACAACCTCAAGCCTGTGACCGA CGCTTTAGTGTGACAAGAGAAAGCTGTGAGACCTC	1499
Db	1201	ACAACCTCAAGCCTGTGACCGA CGCTTTAGTGTGACAAGAGAAAGCTGTGAGACCTC	1260
QY	1500	TATGGCACTAAGAAAGTCCGTGTGTGCCAGATGTGCGAAGCTGATCTCCAA CACGGATGAC	1559
Db	1261	TATGGCACTAAGAAAGTCCGTGTGTGCCAGATGTGCGAAGCTGATCTCCAA CACGGATGAC	1320
QY	1560	GCCCTTGCTTGTCTTTGGGGTCCCTCTTCTGTGAAGCGCAGTTTGACCCGCAAGCAAA	1619
Db	1321	GCCCTTGCTTGTCTTTGGGGTCCCTCTTCTGTGAAGCGCAGTTTGACCCGCAAGCAAA	1380
QY	1620	GAAATTGAGAGGGGATGATACAGCGGAATCCGGACCGCATTTGAGGAAGCCCTGGGACAG	1679
Db	1381	GAAATTGAGAGGGGATGATACAGCGGAATCCGGACCGCATTTGAGGAAGCCCTGGGACAG	1440
QY	1680	CTGGTTTGATGATGAGAGAAGACCCGCGAGGACGCAAGGAGAAAGCAGATGCCATCTAT	1739
Db	1441	CTGGTTTGATGATGAGAGAAGACCCGCGAGGACGCAAGGAGAAAGCAGATGCCATCTAT	1500
QY	1740	GATATGATTTGTTTCCAGACTTTTACTCGGAGCCCAAGAGCTGAGATGTTTATGAC	1560
Db	1501	GATATGATTTGTTTCCAGACTTTTACTCGGAGCCCAAGAGCTGAGATGTTTATGAC	1560
QY	1800	GGGTACGGAATTTCTCGAAGATTCTTTCTCCAAA CAGTTGAGATTGTACACTTCTCT	1859
Db	1561	GGGTACGGAATTTCTCGAAGATTCTTTCTCCAAA CAGTTGAGATTGTACACTTCTCT	1620
QY	1860	GCCAAGTTATGTGCTGACCAAGCTCCGCAAGCCTCCCAAGCCGACAGCAATGAGCATGAC	1919
Db	1621	GCCAAGTTATGTGCTGACCAAGCTCCGCAAGCCTCCCAAGCCGACAGCAATGAGCATGAC	1680
QY	1920	CCCCAGACAGTGAATGCTTACTTACTCTTCCAA CTAAGATGATGTCTTCCCGCTGGC	1979
Db	1681	CCCCAGACAGTGAATGCTTACTTACTCTTCCAA CTAAGATGATGTGTCTTCCCGCTGGC	1740
QY	1980	ATCTCTGACGGCCCCCTTTCTATGTCCCGCAACAACCCCAAGGCCCTTGAA CTTTGGGTGACATC	2039
Db	1741	ATCTCTGACGGCCCCCTTTCTATGTCCCGCAACAACCCCAAGGCCCTTGAA CTTTGGGTGACATC	1800
QY	2040	GATGTGTGATGAGGCGCATGAGTTGACGATGCTTTGATGACCAAGGCGCGAGATATGAC	2099
Db	1801	GATGTGTGATGAGGCGCATGAGTTGACGATGCTTTGATGACCAAGGCGCGAGATATGAC	1860
QY	2100	AAAGAGGGAACCTTGCGGCCCTCTGTGTGAGATGATCCTTGACGACCTTCCGAA CCAAC	2159
Db	1861	AAAGAGGGAACCTTGCGGCCCTCTGTGTGAGATGATCCTTGACGACCTTCCGAA CCAAC	1920
QY	2160	ACGGCTTGCAATGAGAGAA CAGTACAA TCAATACAGGTTCATATGGGAGAGGCTCAACGGC	2219
Db	1921	ACGGCTTGCAATGAGAGAA CAGTACAA TCAATACAGGTTCATATGGGAGAGGCTCAACGGC	1980
QY	2220	CGCCAGACGCTGTGGGAGAA CATTGTCTGACAA CCGGAGGCGCTGAAAGGCTGCTCAACAATGCT	2279
Db	1981	CGCCAGACGCTGTGGGAGAA CATTACTGACAA CCGGAGGCGCTGAAAGGCTGCTCAACAATGCT	2040
QY	2280	TACAAAGCATGTGTGAGAAAGCATGGGAGGAGACGACAACTTGCCAGCCGTGGGCTCAAC	2339

Db	2041	TTACAAAGCTATGCTGAAAGAAAGCATGGGAGAGACAGAACTGGCCAGCCCTGAGGCTTACCC	2100
Qy	2340	AACCAACGAGCTCTTTCTTCGTGGGATTTCGCCAGGTGTGATCTCGATCCGACACCAAG	2399
Db	2101	AACCAACGAGCTCTTCTTCGTGGATTTCGCCAGGTGTGATCTCGATCCGACACCAAG	2160
Qy	2400	AGCTTCACGAGGGGGCTGTGTGACCGACCCCAACAGCCCTGCGCTTCGCGTGTCTGGGC	2459
Db	2161	AGCTTCACGAGGGGGCTGTGTGACCGACCCCAACAGCCCTGCGCTTCGCGTGTCTGGGC	2220
Qy	2460	ACTCTCTCCAACTCCCGTGACTTCCTGTGGGCACTTGGGCTGCCCTGTCCGCTCCCATG	2519
Db	2221	ACTCTCTCCAACTCCCGTGACTTCCTGTGGGCACTTCCGCTGCCCTGTCCGCTCCCATG	2280
Qy	2520	AACCCAGGGGACGCTGTGTGAGTGTGTGACCTGCATCAGAGGGAGAAATGCCAGCTGT	2579
Db	2281	AACCCAGGGGACGCTGTGTGAGTGTGTGACCTGCATCAGAGGGAGAAATGCCAGCTGT	2340
Qy	2580	CACCAAGACTGGGGGACGCTCTCTGCACAAAGCTGTTGCTTGTGGTTGGAGAGCA	2639
Db	2341	CACCAAGACTGGGGGACGCTCTCTGCACAAAGCTGTTGCTTGTGGTTGGAGAGCA	2400
Qy	2640	ATGCAAGCTGGGGCTGGGTCTAGTCCCTCCGCCACAGGTGACATGATGCAGACCCCTGC	2699
Db	2401	ATGCAAGCTGGGGCTGGGTCTAGTCCCTCCGCCACAGGTGACATGATGCAGACCCCTGC	2460
Qy	2700	TCAATTCACACCAATTGTGCTCTGTGGGGGTGCCCCCTGCTCAGCAGAGCCCCCAGC	2759
Db	2461	TCAATTCACACCAATTGTGCTCTGTGGGGGTGCCCCCTGCTCAGCAGAGCCCCCAGC	2520
Qy	2760	ATTCACTGTGTGACATCTTTCGCGTGCACCTGTGCTGTGAGAGAGTCTGGGTGGAGAGC	2819
Db	2521	ATTCACTGTGTGACATCTTTCGCGTGCACCTGTGCTGTGAGAGAGTCTGGGTGGAGAGC	2580
Qy	2820	TTCCCATATGAGAGAGATCTGCC	2841
Db	2581	TTCCCATATGAGAGAGATCTGCC	2602
RESULT 4			
AACT8592			
ID	AACT8592 standard; cDNA; 2602 BP.		
XX			
AC	AACT8592;		
XX			
DT	08-FEB-2001 (first entry)		
DE	Human PR0403 nucleotide sequence SEQ ID NO:525.		
XX			
KM	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;		
KW	expressed sequence tag; detection; cancer; ss.		
XX			
OS	Homo sapiens.		
PN	WO200053756-A2.		
XX			
PD	14-SEP-2000.		
XX			
PF	18-FEB-2000; 2000WO-US004341.		
XX			
PR	08-MAR-1999; 99WO-US005028.		
PR	12-MAR-1999; 99US-0123957P.		
PR	29-MAR-1999; 99US-0126773P.		
PR	21-APR-1999; 99US-0130232P.		
PR	28-APR-1999; 99US-0131445P.		
PR	14-MAY-1999; 99US-0134287P.		
PR	23-JUN-1999; 99US-0141037P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	29-OCT-1999; 99US-0162506P.		
PR	30-NOV-1999; 99WO-US028213.		
PR	02-DEC-1999; 99WO-US028551.		
PR	02-DEC-1999; 99WO-US028565.		





CC comparing the level of expression of a PRO polypeptide in a test sample  
CC of cells from the animal and a control sample indicates the presence of a  
CC higher level of expression in the test sample indicates the presence of a  
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
CC pigs, goats and rabbits but are preferably human. The polypeptide can be  
CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
CC blood, when contacted with it. A specific polypeptide can be used to  
CC stimulate the proliferation or differentiation of chondrocyte cells. The  
CC PRO proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX

Sequence 2602 BP; 577 A; 737 C; 767 G; 521 T; 0 U; 0 Other;

Query Match 72.9%; Score 2461.2; DB 4; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCTGCTTAGAGTATGATGATGATTCAGAGGGGCAAGACAGCTGTAGGCTCACGC 419  
DB 121 CTGGAGACTGACAGCAAGTGGATTCAGAGGGGCAAGACAGCTGTAGGCTCACGC 180  
QY 420 ACCGAGCTGAGAGTGTCTTAGAGAGTCTCTCTACTGCTGCTGACTGCTTCTGGGC 479  
DB 181 ACCGAGCTGAGAGTGTCTTAGAGAGTCTCTCTACTGCTGCTGACTGCTTCTGGGC 240  
QY 480 TGCCTTGAGCCCTAGGGGCTCAGTACCAAGAGACCATCCACACGACTGCTTACA 539  
DB 241 TGCCTTGAGCCCTAGGGGCTCAGTACCAAGAGACCATCCACACGACTGCTTACA 300  
QY 540 GAGGCCGCTGAGTGTGAGTGGGAAATCTGGAGTCCCTGGAGCCGAGGGGTGAGGCC 599  
DB 301 GAGGCCGCTGAGTGTGAGTGGGAAATCTGGAGTCCCTGGAGCCGAGGGGTGAGGCC 360  
QY 600 TGTGAGAGCTTTTACAGTCTCTCTGTGGGGCTGATTTGGAGGAACCCCTGCGCAT 659  
DB 361 TGTGAGAGCTTTTACAGTCTCTCTGTGGGGCTGATTTGGAGGAACCCCTGCGCAT 420  
QY 660 GGGGCTTCTGCTGGAACAACCTTCAACAGCCTCTGGACCAAAACAGGCCATCTGAG 719  
DB 421 GGGGCTTCTGCTGGAACAACCTTCAACAGCCTCTGGACCAAAACAGGCCATCTGAG 480  
QY 720 CACCTGTTGAAAACACACCTTCAACAGAGAGTGAAGCTGAGAGAGAGAGAGAGAG 779  
DB 481 CACCTGTTGAAAACACACCTTCAACAGAGAGTGAAGCTGAGAGAGAGAGAGAGAG 540  
QY 780 TTCTACTATCTTGTCTTACAGTGTGAGCGCATTTGAGAGCTGGAGCCCACTGAGA 839  
DB 541 TTCTACTATCTTGTCTTACAGTGTGAGCGCATTTGAGAGCTGGAGCCCACTGAGA 600  
QY 840 GACCTCATTTGAGAGATTTGGTTGGAACATTCGGGGCCCTGGAGCCAGAGCACTTT 899  
DB 601 GACCTCATTTGAGAGATTTGGTTGGAACATTCGGGGCCCTGGAGCCAGAGCACTTT 660  
QY 900 ATGAGAGTTTGAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959  
DB 661 ATGAGAGTTTGAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 960 ATCAGTCCGAGCTTAAAGATTTCCAGAGAGATTTTACAGAGTGAAGAGAGAGAG 1019  
DB 721 ATCAGTCCGAGCTTAAAGATTTCCAGAGAGATTTTACAGAGTGAAGAGAGAGAG 780  
QY 1020 TTTTGGCTCTGCGGATTTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079  
DB 781 TTTTGGCTCTGCGGATTTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 1080 TATCTGATTTACATGAG 1139  
DB 841 TATCTGATTTACATGAG 900  
QY 1140 GAGCAGATGAGAGAGAGTGTGAGTGTGAGATTCAGCTGGCCATCAGAGTGCAGAG 1199

DB 901 GAGCAGATGAGAGAGTGTGAGTGTGAGATTCAGCTGGCCATCAGAGTGCAGAG 960  
QY 1200 GACACAGGCGGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGGT 1259  
DB 961 GACACAGGCGGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGGT 1020  
QY 1260 CTGGAGCCCTCCATGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1319  
DB 1021 CTGGAGCCCTCCATGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080  
QY 1320 AGTGACTGAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1379  
DB 1081 AGTGACTGAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1140  
QY 1380 ATCAACCGAGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAG 1439  
DB 1141 ATCAACCGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAG 1200  
QY 1440 ACAACCTCAAGCTGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAG 1499  
DB 1201 ACAACCTCAAGCTGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAG 1260  
QY 1500 TATGAGACTAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1559  
DB 1261 TATGAGACTAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1320  
QY 1560 GCGCTTGGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1619  
DB 1321 GCGCTTGGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380  
QY 1620 GAATTTGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAGAGAG 1679  
DB 1381 GAATTTGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAGAGAGAG 1440  
QY 1680 CTGGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1739  
DB 1441 CTGGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1500  
QY 1740 GATATATGATTTTCCAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGTGTGAGTGTGAG 1799  
DB 1501 GATATATGATTTTCCAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGTGTGAGTGTGAG 1560  
QY 1800 GGGTACGAATTTCTGAGATTTCTTCCAAACATTTGATTTGATTTGATTTGATTTGAT 1859  
DB 1561 GGGTACGAATTTCTGAGATTTCTTCCAAACATTTGATTTGATTTGATTTGATTTGAT 1620  
QY 1860 GCCAGATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1919  
DB 1621 GCCAGATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1680  
QY 1920 CCCAGAGATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1979  
DB 1681 CCCAGAGATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740  
QY 1980 ATCTCTCAGAGCCCTTCTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2039  
DB 1741 ATCTCTCAGAGCCCTTCTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800  
QY 2040 GGTGTGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2099  
DB 1801 GGTGTGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1860  
QY 2100 AAAG 2159  
DB 1861 AAAG 1920  
QY 2160 ACAGGCTGTGAGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAG 2219  
DB 1921 ACAGGCTGTGAGAGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAGAG 1980  
QY 2220 CCGCAGAGCTGTGAGAGAGAGATTTTCCAGAGATTTTCCAGAGTGTGAGAGAGAGAG 2279

Db	1991	CGCCAGAGCGCTGGGGGAGAAACATTACTACAAACGGGGGGCTGGAGAGCTGCTACTAAATGCT	2040
Qy	2280	TACAAAGCATG3CTGAGAAAGCATGAGGGAGAGAGACACAACTTGACAGCCGTGG3GCTCAAC	2339
Db	2041	TACAAAGCATG3CTGAGAAAGCATGAGGGAGAGAGACAACTTGACAGCCGTGG3GCTCAAC	2100
Qy	2340	AACCAACAGCTCTTCTTGCTGGGATTTTCCAGAGTGTGTGTCTGGTCCGACACACAG	2339
Db	2101	AACCAACAGCTCTTCTTGCTGGGATTTTCCAGAGTGTGTGTCTGGTCCGACACACAG	2160
Qy	2400	AGCTCTCAGAGGG3CTG3TGACGACACCCCAACAGCCCTGACCGCTTCGCG3TCTG3GC	2459
Db	2151	AGCTCTCAGAGGG3CTG3TGACGACACCCCAACAGCCCTGACCGCTTCGCG3TCTG3GC	2220
Qy	2460	ACTCTCTCAACTCCCGTGACTCTCTGCG3GACCTTGCGCTCCCTGCG3CATG	2519
Db	2221	ACTCTCTCAACTCCCGTGACTCTCTGCG3GACCTTGCGCTCCCTGCG3CATG	2280
Qy	2520	AAACCAAGG3CAGCTGTGTGAGGTGTGTGACCTG3ATCAGGG3AGAAATG3CCAGCTGT	2579
Db	2281	AAACCAAGG3CAGCTGTGTGAGGTGTGTGACCTG3ATCAGGG3AGAAATG3CCAGCTGT	2340
Qy	2580	CACCAAGCTGG3GAGCTGCTCCG3ACAAAGCTGTTGCTCTTG3GTTGG3AGAGACAA	2639
Db	2341	CACCAAGCTGG3GAGCTGCTCCG3ACAAAGCTGTTGCTCTTG3GTTGG3AGAGACAA	2400
Qy	2640	ATGCAAGCTGG3GCTGG3GTCTAGTCCCTCCGCCCAACAG3TGACATGATACAGACCTCC	2699
Db	2401	ATGCAAGCTGG3GCTGG3GTCTAGTCCCTCCGCCCAACAG3TGACATGATACAGACCTCC	2460
Qy	2700	TCAATCACAACATTGTGCTCTGCTTTGG3G3TGCCCTGCTCAGACAGCCCCAAC	2759
Db	2461	TCAATCACAACATTGTGCTCTGCTTTGG3G3TGCCCTGCTCAGACAGCCCCAAC	2520
Qy	2760	ATTCACTGTGACATCTTCCG3TGACACCCCTG3CTG3AGAAAG3TCTGG3TGG3AGGCTAG	2819
Db	2521	ATTCACTGTGACATCTTCCG3TGACACCCCTG3CTG3AGAAAG3TCTGG3TGG3AGGCTAG	2580
Qy	2820	TTCCCATAGAAAGAGTCTGCC	2841
Db	2581	TTCCCATAGAAAGAGTCTGCC	2602
RESULT 6			
ABX78737			
ID	ABX78737	standard; cDNA; 2602 BP.	
XX	AC	ABX78737;	
XX	DT	15-APR-2003 (first entry)	
XX	DE	Human PRO polynucleotide #210.	
XX	KW	Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;	
XX	KW	liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;	
XX	XX	antibody dependent enzyme mediated prodnrg therapy.	
XX	OS	Homo sapiens.	
XX	PN	US2003027272-A1.	
XX	PD	06-FEB-2003.	
XX	PE	21-JUN-2002; 2002US-00176492.	
XX	PR	18-SEP-1997; 97US-0059263P.	
XX	PR	18-SEP-1997; 97US-0059266P.	
XX	PR	17-OCT-1997; 97US-0062250P.	
XX	PR	21-OCT-1997; 97US-0063486P.	
XX	PR	24-OCT-1997; 97US-0063120P.	
XX	PR	28-OCT-1997; 97US-0063540P.	
XX	PR	28-OCT-1997; 97US-0063541P.	

PR	28-OCT-1997	97US-00635444
PR	28-OCT-1997	97US-00635544
PR	29-OCT-1997	97US-00637344
PR	31-OCT-1997	97US-00638700
PR	31-OCT-1997	97US-00641030
PR	13-NOV-1997	97US-00653110
PR	21-NOV-1997	97US-00664120
PR	24-NOV-1997	97US-00664660
PR	24-NOV-1997	97US-00667720
PR	11-DEC-1997	97US-00693350
PR	12-DEC-1997	97US-00694250
PR	17-DEC-1997	97US-00698420
PR	18-DEC-1997	97US-00680170
PR	10-MAR-1998	98US-00774500
PR	11-MAR-1998	98US-00776320
PR	11-MAR-1998	98US-00776490
PR	20-MAR-1998	98US-00788660
PR	20-MAR-1998	98US-00789390
PR	27-MAR-1998	98US-00796480
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PR	01-APR-1998	98US-00803230
PR	01-APR-1998	98US-00803330
PR	08-APR-1998	98US-00804040
PR	08-APR-1998	98US-00810700
PR	08-APR-1998	98US-00811950
PR	15-APR-1998	98US-00818380
PR	21-APR-1998	98US-00826580
PR	21-APR-1998	98US-00826590
PR	22-APR-1998	98US-00827040
PR	22-APR-1998	98US-00827970
PR	28-APR-1998	98US-00832920
PR	28-APR-1998	98US-00833250
PR	29-APR-1998	98US-00834960
PR	29-APR-1998	98US-00834990
PR	29-APR-1998	98US-00835590
PR	05-MAY-1998	98US-00843660
PR	06-MAY-1998	98US-00844140
PR	07-MAY-1998	98US-00846390
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PR	07-MAY-1998	98US-00846430
PR	15-MAY-1998	98US-00855790
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PR	15-MAY-1998	98US-00855820
PR	15-MAY-1998	98US-00857080
PR	18-MAY-1998	98US-00860230
PR	22-MAY-1998	98US-00864960
PR	22-MAY-1998	98US-00865980
PR	28-MAY-1998	98US-00870980
PR	02-JUN-1998	98US-00876090
PR	02-JUN-1998	98US-00877590
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PR	04-JUN-1998	98US-00880280
PR	04-JUN-1998	98US-00880330
PR	04-JUN-1998	98US-00883620
PR	05-JUN-1998	98US-00884670
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PR	05-JUN-1998	98US-00884810
PR	05-JUN-1998	98US-00886210
PR	09-JUN-1998	98US-00886550
PR	10-JUN-1998	98US-00887320
PR	10-JUN-1998	98US-00887380
PR	10-JUN-1998	98US-00887400
PR	10-JUN-1998	98US-00888140
PR	10-JUN-1998	98US-00888620
PR	10-JUN-1998	98US-00888625
PR	11-JUN-1998	98US-00888630

PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089900P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089588P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089988P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
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 KW tumour necrosis factor-alpha release; TNF-alpha release;  
 KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.  
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QY 2700 TCAATCAACCAATTTGCTGCTTTGGGGGTGCTCCCTGCTCAGACAGACCCCAAC 2759  
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RESULT 8  
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ID ACA71189 standard; cDNA; 2602 BP.

AC ACA71189;

DT 02-AUG-2003 (first entry)

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DE Human secreted/transmembrane protein (PRO) cDNA #210.

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KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;

KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

KW tissue typing.

XX

OS Homo sapiens.

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PN US2003032112-A1.

PD 13-FEB-2003.

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PF 21-JUN-2002; 2002US-00176756.

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Best Local Similarity 99.5%; Pred. No. 0; Mismatches 13; Indels 0; Gaps 0;

Matches 2469; Conservative 0;

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QY 420 ACGAGCTGAGCTGCTTTAGACAGTGCCTCTTACTGCTGAGCTGCTTCTGAGC 479  
DB 181 ACGAGCTGAGCTGCTTTAGACAGTGCCTCTTACTGCTGAGCTGCTTCTGAGC 240  
QY 480 TGCCTTGGCCCTTGGGGTCCAGTACCAAGAGCCCATCCCAAGCACTGCTTCTGAGC 539  
DB 241 TGCCTTGGCCCTTGGGGTCCAGTACCAAGAGCCCATCCCAAGCACTGCTTCTGAGC 300  
QY 540 GAGGCTGATTCGAGTGGCTGAGAAATCTGAGTCCCTGAGCCGAGGGGTGAGCCCC 599  
DB 301 GAGGCTGATTCGAGTGGCTGAGAAATCTGAGTCCCTGAGCCGAGGGGTGAGCCCC 360  
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DB 361 TGTGAGACTTTTACCAAGTTCTCTGTGGGGGCTGAGTTGAGAGAACCCCTGCCCCAT 420

QY	660	GGGGGTTTCGCTGGGAACAACCTTCAACAGCCTCTGGGACCAAAACCAAGGCCATATCTGAAG	719
Db	421	GGGGCTTCTCGTGGGAACAACCTTCAACAGCCTCTGGGACCAAAACCAAGGCCATATCTGAAG	480
QY	720	CACCTGCTTGGAAAACCAACCTTCAACCTTCAGCAGTGAAGCTGACAGAAACAACAGCGC	779
Db	481	CACCTGCTTGGAAAACCAACCTTCAACCTTCAGCAGTGAAGCTGACAGAAACAACAGCGC	540
QY	780	TTCTAAGCTATCTTGGCTTCAAGGTGAGCGCATTTGAGAGCTGGGAGCCCTGAGCACTGAGA	839
Db	541	TTCTAAGCTATCTTGGCTTCAAGGTGAGCGCATTTGAGAGCTGGGAGCCCTGAGCACTGAGA	600
QY	840	GACCTCATTTGAGAAATGTTGGGTGGAACATTTACGGGGCCCTGGGACAAGAAACAATCTT	899
Db	601	GACCTCATTTGAGAAATGTTGGGTGGAACATTTACGGGGCCCTGGGACAAGAAACAATCTT	660
QY	900	ATGAGAGTGTGGAAGGACAGTAGCAGGAGCCTTACAGGGCCACCCCATTTCTTCAACGCTTAC	959
Db	661	ATGAGAGTGTGGAAGGACAGTAGCAGGAGCCTTACAGGGCCACCCCATTTCTTCAACGCTTAC	720
QY	960	ATCAGTGGCCGACTCTTAAGAGTTCCAAACAGCAATGTTATCCAGGTGAGCAAGCTTGGGCTC	1019
Db	721	ATCAGTGGCCGACTCTTAAGAGTTCCAAACAGCAATGTTATCCAGGTGAGCAAGCTTGGGCTC	780
QY	1020	TTTTCGGCCCTCTCGGGAGTTAATACTTAACAAGAAATGCGCANTGAGAAAGTGTCTACATGCC	1079
Db	781	TTTTCGGCCCTCTCGGGAGTTAATACTTAACAAGAAATGCGCANTGAGAAAGTGTCTACATGCC	840
QY	1080	TATCTGAGATTACATGAGAGAACTGSGGAGTGCCTGSGGTGGGGCCGCCCACTTCCACGAG	1139
Db	841	TATCTGAGATTACATGAGAGAACTGSGGAGTGCCTGSGGTGGGGCCGCCCACTTCCACGAG	900
QY	1140	GAGCAGATGCAAGCAGGTCTGTGAGTTGAGATACAGCTTGCCAAATCAACAGTGGCCAG	1199
Db	901	GAGCAGATGCAAGCAGGTCTGTGAGTTGAGATACAGCTTGCCAAATCAACAGTGGCCAG	960
QY	1200	GACCAAGCGGCGGAGAGAGAAAGATCTTACCAACAGATGACATTTGGAGCTGCAAGCT	1259
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QY	1260	CTGGAGCCCTCCATGAGACTGGCTTGAATCTCTTCTTTCGCTGTCAACATTTGGAAGTTG	1319
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QY	1320	AGTGAAGCTGTGAGCCTGTGTGTGTATGGAGATTTATTTGACAGAGTGTCAAGAGCTC	1379
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QY	1380	ATCAACCGGCAACGGAACCAAGCATCTGTGAACAATTACCTGATCTGGAACCTGTGTGAAGA	1439
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QY	1440	ACAACCTCAAGGCTGTGAGCCGAGAGCTTTGAGTGTGCAACAAGAGAAAGCTGTGAGACCTC	1499
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QY	1500	TATGCACTTAAGAGATCTGTGTGTGCGAGGTGCGAGACTGTGATCTTCAACACGAGTAC	1559
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QY	1560	GCCCTTGGGCTTTGCTTTGGGGTCCCTCTTCTGTGAAGGCCAGTTTGAACCGGACAACAA	1619
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QY	1620	GAAATTTGCAAGGGAGTATCAAGGGAATCCGGAACCGAATTTGAGGAAGCCCTGGGAAG	1679
Db	1381	GAAATTTGCAAGGGAGTATCAAGGGAATCCGGAACCGAATTTGAGGAAGCCCTGGGAAG	1440
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QY	1980	ATCTGACAGGCCCCCTTCTATGCCCCGACCAACCCCAAGGCTTGAACTTGGTGGCATC	2039
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QY	2040	GCTGTGTCATGCGGCCCATGAGTTTACGCAATGCCCTTTGATGACCAAGGCGCGAATTAGAC	2099
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QY	2100	AAAGAGGGAACTGCGGCCCCCTGTGGCAGAAATAGTCCCTGGCAGGCTTCCGGAACAC	2159
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QY	2160	ACGGCTTGTCATGAGAGAACATGACATCAATCAATACAGGTCATATGGGAGAGGCTCAACGAC	2219
Db	1921	ACGGCTTGTCATGAGAGAACATGACATCAATCAATACAGGTCATATGGGAGAGGCTCAACGAC	1980
QY	2220	CGCCAGACGCTGGGGGAGAAATGTCGTCACACGGGGGGCTGAAAGGCTGCTTACATATCT	2279
Db	1981	CGCCAGACGCTGGGGGAGAAATGTCGTCACACGGGGGGCTGAAAGGCTGCTTACATATCT	2040
QY	2280	TACAAGCATGGCTGAGAAACATGCGGAGGAGGACGCACTGCCAGCCGTGGGGCTCAC	2339
Db	2041	TACAAGCATGGCTGAGAAACATGCGGAGGAGGACGCACTGCCAGCCGTGGGGCTCAC	2100
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QY	2400	AGCTCTCACAGGGGGCTGTGTACCGACCCCAAGCCCTGCCCCGCTTCCGGTGTCTGGGC	2459
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QY	2460	ACTCTCTCAACTCCCGTACCTTCTGTGGGCACTTCCGCTGACCTGTCCGCTCCCCATG	2519
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QY	2580	CACCAAGCTTGTGGGCAAGCTCTTCTGTACAAAGCTGTTTGTCTTGGGTTGGAGAGACAA	2639
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DT 05-AUG-2003 (first entry)  
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KW Human: PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
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PR 23-SEP-1998; 98US-0101477P.  
PR 24-SEP-1998; 98US-0101738P.  
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PR 24-SEP-1998; 98US-0101743P.  
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PR 25-SEP-1998; 98US-0101866P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.

Query Match 72.9%; Score 2461.2; DB 7; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;				
QY	360	CTCTGCTCTAGACTATGTGTGGATTCACAAAGGGGCAAGACAGCTGTAGCTCACGC	419	
DB	121	CTGGAGCTGGGCAACGCTGGGATTCACAAAGGGGCAAGACAGCTGTAGCTCACGC	180	
QY	420	ACGACGTGAGCTGTGCTTAGCAGGTCCTCTCTACTGTGCTGCTGCTCTTCTGGG	479	
DB	181	ACGACGTGAGCTGTGCTTAGCAGGTCCTCTCTACTGTGCTGCTGCTCTTCTGGG	240	
QY	480	TGCTTGTGGCCCTAGGGGTCACAGTACACAGAGACCCTACACAGCCTGCTTACA	539	
DB	241	TGCTTGTGGCCCTAGGGGTCACAGTACACAGAGACCCTACACAGCCTGCTTACA	300	
QY	540	GAGGCTGTGCTTGTGAGTGTGGGAAAAATCTGTGAGTCTCTGAGCCGAGGGGTGAGCCC	599	
DB	301	GAGGCTGTGCTTGTGAGTGTGGGAAAAATCTGTGAGTCTCTGAGCCGAGGGGTGAGCCC	360	
QY	600	TGTGAGGACTTTTACAGTCTCTGCTGTGGGGCTGAGATTGAGAGAAACCCCTGCCGAT	659	
DB	361	TGTGAGGACTTTTACAGTCTCTGCTGTGGGGCTGAGATTGAGAGAAACCCCTGCCGAT	420	
QY	660	GGGCGTTCTGCTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGGCCATCTGAAG	719	
DB	421	GGGCGTTCTGCTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGGCCATCTGAAG	480	
QY	720	CACCTGCTTGAACACACACCTTCACTCCAGCAGTGAAGCTGAGCAGAGAGACACAGCCG	779	
DB	481	CACCTGCTTGAACACACACCTTCACTCCAGCAGTGAAGCTGAGCAGAGAGACACAGCCG	540	
QY	780	TTCTACCTATCTTGCTCCTACAGTGTGAGCGATGAGGAGCTGGGAGCCGACCACTGAGA	839	
DB	541	TTCTACCTATCTTGCTCCTACAGTGTGAGCGATGAGGAGCTGGGAGCCGACCACTGAGA	600	
QY	840	GACCTCATTTGAGAGATTTGTGTGTGGAACATTACGGGGCCCTGGGACCAAGCAATTT	899	
DB	601	GACCTCATTTGAGAGATTTGTGTGTGGAACATTACGGGGCCCTGGGACCAAGCAATTT	660	
QY	900	ATGGAAGTGTGGAAGGCAAGTGAAGGAGCCTACAGGGCCACCCATTTCTTCACTGCTAC	959	
DB	661	ATGGAAGTGTGGAAGGCAAGTGAAGGAGCCTACAGGGCCACCCATTTCTTCACTGCTAC	720	
QY	960	ATCAGTGCAGACTCTAAGAGTTCCAAAGCAATGTTATCCAGGTGAGCAGTCTGGGCTC	1019	
DB	721	ATCAGTGCAGACTCTAAGAGTTCCAAAGCAATGTTATCCAGGTGAGCAGTCTGGGCTC	780	
QY	1020	TTTCTGCCCTCTGGGATTACTTAACAAGAACTGCCAATGAGAAAGTCTCACTGCC	1079	
DB	781	TTTCTGCCCTCTGGGATTACTTAACAAGAACTGCCAATGAGAAAGTCTCACTGCC	840	
QY	1080	TATCTGATTTACATGAGAGAACTGGGGATGCTGTGGGTGGGGCCCACTTCCAGAGG	1139	
DB	841	TATCTGATTTACATGAGAGAACTGGGGATGCTGTGGGTGGGGCCCACTTCCAGAGG	900	
QY	1140	GAGCAGATGAGAGGCTGTGAGTGTGAGATACAGCTGGCCAACTACAGTGGCCGAG	1199	
DB	901	GAGCAGATGAGAGGCTGTGAGTGTGAGATACAGCTGGCCAACTACAGTGGCCGAG	960	
QY	1200	GACCAAGCGGCGAGAGAGAGATCTACCAAGATGAGATTTGAGAGCTGAGGCT	1259	
DB	961	GACCAAGCGGCGAGAGAGAGATCTACCAAGATGAGATTTGAGAGCTGAGGCT	1020	
QY	1260	CTGGCCCTCTCATGAGTGTGGCTTGAATTCCTTCTTCTGCTGTCACTATGAGATTG	1319	
DB	1021	CTGGCCCTCTCATGAGTGTGGCTTGAATTCCTTCTTCTGCTGTCACTATGAGATTG	1080	
QY	1320	AGTGACTTGAAGCTGTGTGTGTGTATGAGATTTATTTGAGAGAGGTGTGAGAGCTC	1379	
DB	1081	AGTGACTTGAAGCTGTGTGTGTGTATGAGATTTATTTGAGAGAGGTGTGAGAGCTC	1140	
QY	1380	ATCAACCGGAGGAGCAAGCATCTTGAACAAATTTACTGTGAACCTGTGCAAAAG	1439	
DB	1141	ATCAACCGGAGGAGCAAGCATCTTGAACAAATTTACTGTGAACCTGTGCAAAAG	1200	

QY	1440	ACAACCTCAAGCCTGGAGCCGAGCCTTGAAGTCTGACAAAGAGAGTGTGAGACCTTC	1499	
DB	1201	ACAACCTCAAGCCTGGAGCCGAGCCTTGAAGTCTGACAAAGAGAGTGTGAGACCTTC	1260	
QY	1500	TATGCACTAAGAAGTCTGTGTGCGAGAGTGGCAGACCTGTACTTCAACAGATGAC	1559	
DB	1261	TATGCACTAAGAAGTCTGTGTGCGAGAGTGGCAGACCTGTACTTCAACAGATGAC	1320	
QY	1560	GCCCTTGGCTTTGCTTTGGGGTCTCTTCTGTGAAGGCCAGTTTGAACGGCAAGCAAA	1619	
DB	1321	GCCCTTGGCTTTGCTTTGGGGTCTCTTCTGTGAAGGCCAGTTTGAACGGCAAGCAAA	1380	
QY	1620	GAAATTTGAGAGAGGATGATTCAGCGAAATCCCGAACCGCATTTTGAAGAGGCCCTGGAGAG	1679	
DB	1381	GAAATTTGAGAGAGGATGATTCAGCGAAATCCCGAACCGCATTTTGAAGAGGCCCTGGAGAG	1440	
QY	1680	CTGGTTTGAATGATGAGAGAACCCGCGAGGCGAGCCCAAGAGAGAGATGCTATAT	1739	
DB	1441	CTGGTTTGAATGATGAGAGAACCCGCGAGGCGAGCCCAAGAGAGAGATGCTATAT	1500	
QY	1740	GATATGATTTGTTTCCCAAGCTTTATCTGAGGCCCAAGAGCTGATGATTTATGAC	1799	
DB	1501	GATATGATTTGTTTCCCAAGCTTTATCTGAGGCCCAAGAGCTGATGATTTATGAC	1560	
QY	1800	GGGTAGAAATTTCTGAAGATTTCTTCTTCAAAAGATTTGATCAACTTCTCT	1859	
DB	1561	GGGTAGAAATTTCTGAAGATTTCTTCTTCAAAAGATTTGATCAACTTCTCT	1620	
QY	1860	GCCAAAGTTATGGCTGACAGAGCTCCGCAAGCCTCCAGCCGAGACCAAGTGAAGATGAC	1919	
DB	1621	GCCAAAGTTATGGCTGACAGAGCTCCGCAAGCCTCCAGCCGAGACCAAGTGAAGATGAC	1680	
QY	1920	CCCCAGACAGTGAATCTTACTTCACTTCAAGATGAGATGCTTCTCCGCTGGC	1979	
DB	1681	CCCCAGACAGTGAATCTTACTTCACTTCAAGATGAGATGCTTCTCCGCTGGC	1740	
QY	1980	ATCCTGCAAGCCCTCTTATGCTGCGCAACACCCCAAGCCCTGAACTTGGTGGCCTC	2039	
DB	1741	ATCCTGCAAGCCCTCTTATGCTGCGCAACACCCCAAGCCCTGAACTTGGTGGCCTC	1800	
QY	2040	GGTGTGATGAGGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	2099	
DB	1801	GGTGTGATGAGGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	1860	
QY	2100	AAAAGAGGAACTGTGGGCTCTGTGTGAGAGATGAGTCTGTGGAGCTTCCGGAACAC	2159	
DB	1861	AAAAGAGGAACTGTGGGCTCTGTGTGAGAGATGAGTCTGTGGAGCTTCCGGAACAC	1920	
QY	2160	ACGGCTGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2219	
DB	1921	ACGGCTGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1980	
QY	2220	CGCAGAGCCTGTGGGAGAACTTGTGTAACAAGGGGGCTGAAGGCTCTTCAATGCT	2279	
DB	1981	CGCAGAGCCTGTGGGAGAACTTGTGTAACAAGGGGGCTGAAGGCTCTTCAATGCT	2040	
QY	2280	TACAAAGCATGCTGAGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2339	
DB	2041	TACAAAGCATGCTGAGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2100	
QY	2340	AACCAACAGCTCTTCTGCTGAGATTTGCGCAGAGTGTGTGCTGCTGCGCAACAAGAG	2399	
DB	2101	AACCAACAGCTCTTCTGCTGAGATTTGCGCAGAGTGTGTGCTGCTGCGCAACAAGAG	2160	
QY	2400	AGCTCTCAAGAGAGGCTGTGAGCCGACCCCAAGCCTGCGCTTCCGCTGTGCTGAGC	2459	
DB	2161	AGCTCTCAAGAGAGGCTGTGAGCCGACCCCAAGCCTGCGCTTCCGCTGTGCTGAGC	2220	
QY	2460	ACTCTCTCAACTCCCGTGAATTTCTGTGGGCACTTGTGGCTGCTGTGCTGCTGCTGCTG	2519	
DB	2221	ACTCTCTCAACTCCCGTGAATTTCTGTGGGCACTTGTGGCTGCTGTGCTGCTGCTGCTG	2280	



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Query Match	72.9%	Score 2461.2;	DB 7;	Length 2602;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 2469;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;

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PR 06-OCT-1998; 98US-0103258P.  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 121 CTGGAGACTGGACGACAGCTGGGATTCAGAGGGGACAGAGAGCTTTAGGCTCAGCG 180  
QY 420 ACGCAGCTGAGAGCTGCTTTAGAGAGTCCCTCTCTACTGCTGCTGCTGCTCTTGGG 479  
DB 181 ACCGAGCTGAGAGCTGCTTTAGAGAGTCCCTCTCTACTGCTGCTGCTGCTCTTGGG 240  
QY 480 TGCCTTGTGGCCCTTAGGGGTCAGTACCAAGAGAGCCCATCCCAAGAGAGCTCTTACA 539  
DB 241 TGCCTTGTGGCCCTTAGGGGTCAGTACCAAGAGAGCCCATCCCAAGAGAGCTCTTACA 300  
QY 540 GAGGCTGATTCGAGTGGCTGGAATAATCTGGAGTCCCTGAGCCGAGGGGTGAGGCC 599  
DB 301 GAGGCTGATTCGAGTGGCTGGAATAATCTGGAGTCCCTGAGCCGAGGGGTGAGGCC 360  
QY 600 TGTGAGAGCTTTTACAGATTCTCTGTGGGGGCTGATTCGAGAGAAACCCCTGCGCAT 659  
DB 361 TGTGAGAGCTTTTACAGATTCTCTGTGGGGGCTGATTCGAGAGAAACCCCTGCGCAT 420  
QY 660 GGGGCTTCTGCTGGAACACCTTCAACAGGCTCTGGAACCAAAACAGGGCATATGAG 719  
DB 421 GGGGCTTCTGCTGGAACACCTTCAACAGGCTCTGGAACCAAAACAGGGCATATGAG 480  
QY 720 CACTGCTTGAACACACCTTCAACTCCAGAGTGAAGTGAAGTGAAGAGACAGAGCG 779  
DB 481 CACTGCTTGAACACACCTTCAACTCCAGAGTGAAGTGAAGTGAAGAGACAGAGCG 540  
QY 780 TTTCTACTATCTTCCCTACAGTGGAGCGCATTTGAGAGGCTGGAGCCAGCACTGAGA 839  
DB 541 TTTCTACTATCTTCCCTACAGTGGAGCGCATTTGAGAGGCTGGAGCCAGCACTGAGA 600  
QY 840 GACTCTATTTGAAGAGATTTGGTGGTGGAGCATTAACGGGGGCTGGAGCCAGCACTTT 899  
DB 601 GACTCTATTTGAAGAGATTTGGTGGTGGAGCATTAACGGGGGCTGGAGCCAGCACTTT 660  
QY 900 ATGAGAGTGTGAAGAGAGTGAAGAGAGAGCTTACAGGGGCAACCCCATTTCTACCGTTC 959  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;

Best Local Similarity 99.5%; Pred No. 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 420 AGGAGCTGAGAGCTGCTTTAGCAGAGGCTCTTACTGCTGCTGCTTACCTTTCTGGGC 479  
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DB 241 TGGCTTGTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 300  
QY 540 GAGGCTGATTCAGAGTGGGCTGGAAGATCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAG 599  
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QY 600 TGTGAGAGCTTTTACCAAGTTCCTGTGGGCTGGAAGTCTTGAAGTCTTGAAGTCTTGAAG 659  
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QY 660 GGGGCTTGTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 719  
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QY 720 CACCTGCTTGAAGACCACTTCAATCTGAGAGTGAAGCTTGAAGACCACTTGAAGACCA 779  
DB 481 CACCTGCTTGAAGACCACTTCAATCTGAGAGTGAAGCTTGAAGACCACTTGAAGACCA 540  
QY 780 TTCTACTATCTTGGCTTACAGGTGAGGCGCATTTGAGAGTGGAGCGGCGGAGCACTGAGA 839  
DB 541 TTCTACTATCTTGGCTTACAGGTGAGGCGCATTTGAGAGTGGAGCGGCGGAGCACTGAGA 600  
QY 840 GACCTATTGAGAGATTTGATTTGAACATTTACGGGCGCTTGGGACCACTTGAAGCACTTT 899  
DB 601 GACCTATTGAGAGATTTGATTTGAACATTTACGGGCGCTTGGGACCACTTGAAGCACTTT 660  
QY 900 ATGAGAGTGTGAAGGCACTGAGGAGCACTTCAAGGGGCACTTCAAGGAGCACTTCAAGG 959

Db	661	ATGAGAGTGTGAAGCAGTACAGAGGACCTACAGGGGCCACCCATTCTTACACCGTCTAC	720
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Qy	1020	TTTCTGCCCCCTCTCCGGGATTACTACTTAAACGAACTGGCATTGAGAAAGTCTCACTGCC	1079
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Qy	1080	TATCTGATTTACATGAGAGAACTGGGGAGTGCCTGCTGGGTGGGGCCGCCACTCCACGAG	1139
Db	841	TATCTGATTTACATGAGAGAACTGGGGAGTGCCTGCTGGGTGGGGCCGCCACTCCACGAG	900
Qy	1140	GAGCAGATGACAGCAGTGTCTGAGTTGGAGATACAGCTGGCCAACTACAGTGGCCCGAG	1139
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Qy	1200	GACCAAGCCGCGGACAGAGAGAAATCTAACCAAGATGAGCATTTCCGAGCTGACGCT	1259
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Db	1921	ACGGCTGTCATGAGAGAAACAGTCAATCAATATCAAGGTCAATGGGAGAGGCTCAACGGC	1980
QY	2220	CGCCAGACGCTGGGGGGGGAACATTTGCTGACAAACGGGGGGGCTGAAGGCTGCTTAATATGCT	2279
Db	1981	CGCCAGACGCTGGGGGGGGAACATTTGCTGACAAACGGGGGGGCTGAAGGCTGCTTAATATGCT	2040
QY	2280	TACAAAGCATGGCTGAGAAAGCATGGGAGAGAGAGCACTGACGAGCCGTGGGCTCAAC	2339
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QY	2520	AACCCAGGGCAGCTGTGTGAGGTGTGTGACCTGTGATCAAGGGAGAAATGCCAAGCTGT	2579
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QY	2700	TCAATCAACACATTTGTGCTCTGCTTTGGGGGTGCCCCCTGCTCAAGACAGCCCCCAAC	2759
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DT	11-AUG-2003	(first entry)	
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XX	Human; PRO; secreted protein; transmembrane protein; TNF-alpha;		
KM	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KM	chondrocyte; proliferation; differentiation; cartilage disorder;		
KM	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KM	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		

KW liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritis; vulnery; gene therapy; gene; ss.  
OS Homo sapiens.  
XX US2003027264-A1.  
XX  
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QY 2521 ACCGAGGCGAGCTGTGAGAGTGTGAGACCTGAGTCAGGGGAGAAATGCCAGCTGTC 2580  
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QY 2701 CAATCAACCAATTGTGCTGTGCTTGGGGGTGCGGCTGCTCAGAGAGCCCAACCA 2760  
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RESULT 2  
US-10-453-764-1  
; Sequence 1, Application US/10453764

Publication No. US20030232044A1  
GENERAL INFORMATION:  
APPLICANT: White, David  
TITLE OF INVENTION: USE FOR ENDOTHELIN CONVERTING ENZYME 2  
TITLE OF INVENTION: (BCE-2) IN THE DIAGNOSIS AND TREATMENT OF METABOLIC  
FILE REFERENCE: MP102-266P1RM  
CURRENT APPLICATION NUMBER: US/10/453,764  
PRIOR FILING DATE: 2003-06-03  
PRIOR FILING DATE: 2002-06-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 3138  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (49) ... (2346)  
US-10-453-764-1  
Query Match 88.5%; Score 2988.4; DB 16; Length 3138;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 3137; Conservative 0; Mismatches 1; Indels 138; Gaps 1;  
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Qy 3306 TAGACCTGTGTGCAATTAACAGACATGATCCGTC 3341  
Db 3103 TAGACCTGTGTGCAATTAACAGACATGATCCGTC 3138

RESULT 3  
US-09-978-295A-525  
Sequence 525, Application US/09978295A  
Patent No. US2002015606A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guirney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mackey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064429  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 9; Length 2602;  
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Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 121 CTGGAGCTGGAGCAACGTGGGATTCAGAAAGGAGCAAGACAGCTGTAGGCTCAGGC 180

QY 420 AGGAGCTGAGACTGGCTTTAGAGGTGCTCTTACTGCTGGCTGCACTGCTTGTGGGC 479  
DB 181 AGCAGCTGAGCTGGCTTTAGAGGTGCTCTTACTGCTGGCTGCACTGCTTGTGGGC 240

QY 480 TGCTTGTGGCCCTAGGGGTCCAGTACACAGAGACCCATCCACAGCACTGCTTACA 539  
DB 241 TGCTTGTGGCCCTAGGGGTCCAGTACACAGAGACCCATCCACAGCACTGCTTACA 300

QY 540 GAGGCTGCAATTCAGTGGCTGGAATAATCTGAGTCCCTGGAACCGAGGGGTAGCCCC 599  
DB 301 GAGGCTGCAATTCAGTGGCTGGAATAATCTGAGTCCCTGGAACCGAGGGGTAGCCCC 360

QY 600 TGTGAGAGCTTTTACCAAGTTCCTGTGGGGCTGGATTCGAGAGAACCCCTGGCCGAT 659  
DB 361 TGTGAGAGCTTTTACCAAGTTCCTGTGGGGCTGGATTCGAGAGAACCCCTGGCCGAT 420

QY 660 GGGCGTTCTGCTGGAACAACCTTCAACAGCTCTGGGACCAAAACAGGCCATCTAGAG 719  
DB 421 GGGCGTTCTGCTGGAACAACCTTCAACAGCTCTGGGACCAAAACAGGCCATCTAGAG 480

QY 720 CACCTGCTTGAACAACCACTTCAACCTCAGAGTGAAGCTGAGCAAGAACACAGCGCC 779  
DB 481 CACCTGCTTGAACAACCACTTCAACCTCAGAGTGAAGCTGAGCAAGAACACAGCGCC 540

QY 780 TTCTACCTATCTTGCTTACAGGTGAGGAGCATTTGAGAGCTGGGACCCAGCACTAGAG 839  
DB 541 TTCTACCTATCTTGCTTACAGGTGAGGAGCATTTGAGAGCTGGGACCCAGCACTAGAG 600

QY 840 GACCTCATTTGAGAGATTTGGTGGTGAACATTTACGGGCGCTGGGACCAAGAACATTT 899  
DB 601 GACCTCATTTGAGAGATTTGGTGGTGAACATTTACGGGCGCTGGGACCAAGAACATTT 660

QY 900 ATGAGAGTGTGAAGGACAGTGAAGGACCTTACAGGGCCACCCCATTTTACCGTTAC 959  
DB 661 ATGAGAGTGTGAAGGACAGTGAAGGACCTTACAGGGCCACCCCATTTTACCGTTAC 720

QY 960 ATGAGGCGGACCTTACAGGATTCACACAGCATTTATCAGGTGAGACCACTGGGCTC 1019  
DB 721 ATGAGGCGGACCTTACAGGATTCACACAGCATTTATCAGGTGAGACCACTGGGCTC 780

QY 1020 TTTCTGCCCTCTGGGATTTACTTAAACAGAACTGCCAATGAGAAATGCTCACTGCC 1079  
DB 781 TTTCTGCCCTCTGGGATTTACTTAAACAGAACTGCCAATGAGAAATGCTCACTGCC 840

QY 1080 TATCTGATTTACATGAGAGAACTGGGAGTCTGCTGGGTGGGCGCCACTTCAAGAGG 1139  
DB 841 TATCTGATTTACATGAGAGAACTGGGAGTCTGCTGGGTGGGCGCCACTTCAAGAGG 900

QY 1140 GAGCAATGACAGAGGTGCTGAGTGGAGTACAGCTGGCCAACTCAAGTGCCCAAG 1199  
DB 901 GAGCAATGACAGAGGTGCTGAGTGGAGTACAGCTGGCCAACTCAAGTGCCCAAG 960

QY 1200 GACCAAGCGGCGAGCAGAGAGAGATCTACCAACAGATGAGATTTGAGAGTCAAGGCT 1259



FILE REFERENCE: P2630PIC27  
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PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 03/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.3%; Score 2461.2; DB 9; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCTGCTAGAGCTATGTTGGGATTCAGAAAGGGGCAAGACAGCTGTTAGGCTACGCC 419  
DB 121 CTGGAGCTGGCGAGCAAGTGGGATTCAGAAAGGGGCAAGACAGCTGTTAGGCTACGCC 180  
QY 420 AGCAGCTGGAGGCTGCTTGAAGGCTCTCTAAGTGGCTGCACTTGGGGC 479  
DB 181 ACCAGCTGGAGGCTGCTTGAAGGCTCTCTAAGTGGCTGCACTTGGGGC 240  
QY 480 TGCCTTGGCCCTAGAGGCTCAGTACACAGAGCCCATCCACAGCACTGCTTACA 539  
DB 241 TGCCTTGGCCCTAGAGGCTCAGTACACAGAGCCCATCCACAGCACTGCTTACA 300  
QY 540 GAGGCTGCATTTGAGTGGCTGGAATAATCTGAGTCCCTGGAACGAGGGGTGAGCCCC 599  
DB 301 GAGGCTGCATTTGAGTGGCTGGAATAATCTGAGTCCCTGGAACGAGGGGTGAGCCCC 360  
QY 600 TGTGAGGACCTTTACAGATTCCTGTTGGGGGCTGGAATTCGAGGAACCCCTGCCGAT 659  
DB 361 TGTGAGGACCTTTACAGATTCCTGTTGGGGGCTGGAATTCGAGGAACCCCTGCCGAT 420  
QY 660 GGGGCTTCTGCTGGAACACTTCAACAGCTCTGGAGCCAAACAGGCTCATCTGAAG 719  
DB 421 GGGGCTTCTGCTGGAACACTTCAACAGCTCTGGAGCCAAACAGGCTCATCTGAAG 480  
QY 720 CACCTGCTGAAAACACACCTTCAACTCCAGAGTGAAGCTGAGCAAGAACACAGCGC 779  
DB 481 CACCTGCTGAAAACACACCTTCAACTCCAGAGTGAAGCTGAGCAAGAACACAGCGC 540  
QY 780 TTCTACCTATCTGCTTACAGGAGGAGGAGGATTTAGAGCTGGAGCCAGGCTGAGAG 839  
DB 541 TTCTACCTATCTGCTTACAGGAGGAGGAGGATTTAGAGCTGGAGCCAGGCTGAGAG 600  
QY 840 GACCTCATTTAGAAAGATTTGGTGTGAAACATTAACGGGGCCTTGGAGCAAGCACTTT 899  
DB 601 GACCTCATTTAGAAAGATTTGGTGTGAAACATTAACGGGGCCTTGGAGCAAGCACTTT 660

QY	900	ATGAGAGGTTGAAGGCAAGTGCAGAGGACCTTAACAGGGGCAACCCATTCCTTCAAGGTCATC	959
Db	661	ATGAGAGGTTGAAGGCAAGTGCAGAGGACCTTAACAGGGGCAACCCATTCCTTCAAGGTCATC	720
QY	960	ATCAAGTCCGACCTTAAGAGTTTCCAAACGACATGTTATCCAGGTGAGCAAGTCTGGGCTC	1019
Db	721	ATCAAGTCCGACCTTAAGAGTTTCCAAACGACATGTTATCCAGGTGAGCAAGTCTGGGCTC	780
QY	1020	TTTCTGGCCCTCCGGGATTTACTACTTAACGAAGCTGCAATGAGAAAGTCTCACTGGC	1079
Db	781	TTTCTGGCCCTCCGGGATTTACTACTTAACGAAGCTGCAATGAGAAAGTCTCACTGGC	840
QY	1080	TATCTGATTTACATGAGAGAACTGGGGATGCTGCTGGGTGGGCGGCCCACTCCACGAGG	1139
Db	841	TATCTGATTTACATGAGAGAACTGGGGATGCTGCTGGGTGGGCGGCCCACTCCACGAGG	900
QY	1140	GAGCAGATGCAAGCTGCTGAGTTGGAGATACAGCTGGCCATCATCAAGTCCCCAG	1199
Db	901	GAGCAGATGCAAGCTGCTGAGTTGGAGATACAGCTGGCCATCATCAAGTCCCCAG	960
QY	1200	GACCAAGCGGCGGAGAGAGAAATCTACCAAGAATGAGCAATTTGGAGCTCAGAGCT	1259
Db	961	GACCAAGCGGCGGAGAGAGAAATCTACCAAGAATGAGCAATTTGGAGCTCAGAGCT	1020
QY	1260	CTGGGCGCTTCATGAGACTGGCTTGAGTTCTGTCTTTCTTGCTGTCAACATTGAGTTG	1319
Db	1021	CTGGGCGCTTCATGAGACTGGCTTGAGTTCTGTCTTTCTTGCTGTCAACATTGAGTTG	1080
QY	1320	AGTAGCTCTGAGCCGTGTGTGTGTATGAGATGATTTATTTGCAAGAGTGTCAAGGCTC	1379
Db	1081	AGTAGCTCTGAGCCGTGTGTGTGTATGAGATGATTTATTTGCAAGAGTGTGTCAAGGCTC	1140
QY	1380	ATCAACCGCACGGAACCAAGCATCTCTGAACATTAACCTGATCTGGAACCTGTGCAAAAG	1439
Db	1141	ATCAACCGCACGGAACCAAGCATCTCTGAACATTAACCTGATCTGGAACCTGTGCAAAAG	1200
QY	1440	ACAACCTCAAGCTCTGAGCCGACGCTTTGAGTCTGACAAAGAAAGTCTCTGAGACCTC	1499
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QY	1500	TATGCACTAAGAAATCCTGTGTGTGCGAGGTGGCAGACCTGCATCTCAACACGAGATGAC	1559
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QY	1560	GCCCTTGCTTGTCTTTGGGGTCCCTCTCTTGTAAGGCCAAGTGTGACCGGCAAAAGCAA	1619
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Db	1381	GAAATTTGCAAGGGGATGATGTCAGGCAATTCGGGACCGGATTTGAGGAGAGCCCTGGGACAG	1440
QY	1680	CTGGTTTGGATGATGAGAAAGACCCGCGACAGGACGCAAGAGAAAGCAGATGCCATCTAT	1739
Db	1441	CTGGTTTGGATGATGAGAAAGACCCGCGACAGGACGCAAGAGAAAGCAGATGCCATCTAT	1500
QY	1740	GATATGATTTGTTTCCCAAGCTTTATCTGTGAGCCCAAGAGCTGAGATGATTTATGAC	1799
Db	1501	GATATGATTTGTTTCCCAAGCTTTATCTGTGAGCCCAAGAGCTGAGATGATTTATGAC	1560
QY	1800	GGGTACGAAATTTCTGAGAAATCTTCTTCTCCAAAACATGTTGAATTTGTACAACCTCTCT	1859
Db	1561	GGGTACGAAATTTCTGAGAAATCTTCTTCTCCAAAACATGTTGAATTTGTACAACCTCTCT	1620
QY	1860	GCCAAAGTTATGGCTGACCAAGCTCCGCAAGCCTCCAGCCGACCAAGCAATGAGCATGAC	1919
Db	1621	GCCAAAGTTATGGCTGACCAAGCCTCCGCAAGCCTCCAGCCGACCAAGCAATGAGCATGAC	1680
QY	1920	CCCCAGACAGTGAATGACCTACTACCTTCCAACTAAGATGAGATGCTTCCCGCTGGC	1979
Db	1681	CCCCAGACAGTGAATGACCTACTACCTTCCAACTAAGATGAGATGCTTCCCGCTGGC	1740

[illegible]

RESULT 6  
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Sequence 525, Application US/09999832A  
Publication NO. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Borstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerilsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavan, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
PRIOR FILING DATE: 2001-10-24  
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Query Match 72.9%; Score 2461.2; DB 9; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0; Mismatches 13; Indels 0; Gaps 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 181 ACGAGCTGAGAGCTGATCTTAGCAGGTCCTCTCTACTGCTGCTGACCTGCTTGGGC 240  
QY 480 TGCTTGTGGCCCTTAGGGGTCAGTACCAAGAGACCCATCCCAACAGACTGCTTACA 539  
DB 241 TGCTTGTGGCCCTTAGGGGTCAGTACCAAGAGACCCATCCCAACAGACTGCTTACA 300  
QY 540 GAGGCTGCAATTGAGTGGCTGAGAAATCCTGAGTCCCTGACCGAGGGGATGAGCCC 599  
DB 301 GAGGCTGCAATTGAGTGGCTGAGAAATCCTGAGTCCCTGACCGAGGGGATGAGCCC 360  
QY 600 TGTGAGACTTTTACAGTTCTCTGTGAGGGCTGATTGAGAGAACCCCTGCGCAT 659  
DB 361 TGTGAGACTTTTACAGTTCTCTGTGAGGGCTGATTGAGAGAACCCCTGCGCAT 420  
QY 660 GGGGTTTCTGCTGGAACCTTCAAGAGCTCTGGGACCAAAACGAGGCTATCTAAG 719  
DB 421 GGGGTTTCTGCTGGAACCTTCAAGAGCTCTGGGACCAAAACGAGGCTATCTAAG 480

QY 720 CACCTGCTGAAAAACACACTTCACTCCAGAGTGAAGTGAAGAGACAGAGCC 779  
DB 481 CACTGCTTGAACACACACTTCACTCCAGAGTGAAGTGAAGAGACAGAGCC 540  
QY 780 TTCTACCTATCTTCCCTTACAGGTGAGCGCATTTGAGAGCTGGAGCCCACTGAGA 839  
DB 541 TTCTACCTATCTTCCCTTACAGGTGAGCGCATTTGAGAGCTGGAGCCCACTGAGA 600  
QY 840 GACCTATGAGAAATGTTGTTGGAACATTAAGGGGCTCTGGAGCCAGGACAACTTT 899  
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QY 900 ATGAGAGTTGTAAGGCACTAGAGGACCTTCAAGGGCCACCCCACTTCTTCACTGAC 959  
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QY 960 ATCAGTCCGACTTAAAGATTCCAAACAGCAATGTTATCAGGTGACCAAGTCTGGCTC 1019  
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QY 1140 GAGCAGATGACAGAGTCTGAGATTGAGATTCAGCTGGCCCACTCAAGTCCCGAG 1199  
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Qy	1980	ATCTGACAGGCCCCCTTCTATGCGCGCAACACCCCAAGGCGCTTAACTTTCGATGACATC	2039
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Qy	2160	ACGGCTTCATGAGAGGAACAGTACATCAATACAGATCAATGAGGGAAGAGGCTCAAGGCG	2219
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Db	2041	TACAAAGCATGGCTGAGAAAGCATGGGAGAGACAGCACTGCCAGCGTGGGCTCAC	2100
Qy	2340	AACCAACCAAGCTCTTCTGATGGGAATTTGCCAGAGTGGTGTGCTCGATCCGACACCAAG	2399
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Qy	2400	AGCTCTCAAGAGGGGCTGATGACCGACCCCAACAGCCCTGCGCGCTTCCGAGTGTGGGC	2455
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Qy	2580	CACCAAGACCTGAGGAGCTCTCTCTGACCAAGAGTGTTCCTCTTGGGTTGGGAGGAAGCA	2639
Db	2341	CACCAAGACCTGAGGAGCTCTCTCTGACCAAGAGTGTTCCTCTTGGGTTGGGAGGAAGCA	2400
Qy	2640	ATGCAAGCTGGGCTGGGTCTAGTCCCTTCCCGCCCAACAGATGACATGATGACAGACCTTCC	2699
Db	2401	ATGCAAGCTGGGCTGGGTCTAGTCCCTTCCCGCCCAACAGATGACATGATGACAGACCTTCC	2460
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Db	2461	TCAATCAACCAATTGTGCTCTGCTTTGGGGGTGCGCTGCTCTCAGACAGACCCCAAC	2520
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Db	2521	ATTACAGTGCATCTTTCCGATGACACCTGCTGAGGAAGAGGCTCGGGTGGGGAGGCGAG	2580
Qy	2820	TTCCCATGAGAGGAGTCTGCC 2841	
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavina, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCTGCTTAGAGCTATGATGAGATTCAGAAAGGAGCAAGACGTTAGAGCTTACGC 419  
DB 121 CTGGAGAGCTGGAGCAAGCTGGGATTCAGAAAGGAGCAAGACGTTAGAGCTTACGC 180  
QY 420 ACGCAGCTGAGGTGATCTTAGAGGTGCTCTTACTGCTGAGCTTGCATTCGTCGGC 479  
DB 181 ACGCAGCTGAGGTGATCTTAGAGGTGCTCTTACTGCTGAGCTTGCATTCGTCGGC 240  
QY 480 TGCCCTGTGAGCCCTTAGAGGCTCAGTACACAGAGACCCATCCACAGCACTGCTTAA 539  
DB 241 TGCCCTGTGAGCCCTTAGAGGCTCAGTACACAGAGACCCATCCACAGCACTGCTTAA 300  
QY 540 GAGGCTGATTCGAGTGGCTGAGAAATCTGGAATCCCTGGAACGAGGCTGAGCCCC 599

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Db 301 |||||GAGGCGTGCATGTGAGTGGCTGGAATAATCTGGAGTCCCTGGACCGAGGGGTGAGCCCC 360
Qy 600 |||||TGTGAGGACTTTTAAACAGTTTCTCTGTGGGGGCTGTGATTTGGAGAAACCCCTGCCCCGAT 659
Db 361 |||||TGTGAGGACTTTTAAACAGTTTCTCTGTGGGGGCTGTGATTTGGAGAAACCCCTGCCCCGAT 420
Qy 660 |||||GGGGGTTCTGGCTGGAAACACCTTCAACAGGCTCTGGGACCAAAACCAAGGCGATCTGAG 719
Db 421 |||||GGGGGTTCTGGCTGGAAACACCTTCAACAGGCTCTGGGACCAAAACCAAGGCGATCTGAG 480
Qy 720 |||||CACCTGCTTGAACCAACACCTTCAACAGGCTCTGGGACCAAAACCAAGGCGATCTGAG 779
Db 481 |||||CACCTGCTTGAACCAACACCTTCAACAGGCTCTGGGACCAAAACCAAGGCGATCTGAG 540
Qy 780 |||||TTTCTACTATCTTGGCTTCAAGGTGAGGCGCATTTGAGAGCTGGAGCCCAAGCCACTGAGA 839
Db 541 |||||TTTCTACTATCTTGGCTTCAAGGTGAGGCGCATTTGAGAGCTGGAGCCCAAGCCACTGAGA 600
Qy 840 |||||GACCTCATTTGAGAGATTGGTGGTGGACATTAACGGGGGCTGGGACCAAGCAACTTT 899
Db 601 |||||GACCTCATTTGAGAGATTGGTGGTGGACATTAACGGGGGCTGGGACCAAGCAACTTT 660
Qy 900 |||||ATGAGGTGTGTGAAGGCGATGAGGAGGACCTTACAGGCGCAACCCCATTTCTTCAACCGTCTAC 959
Db 661 |||||ATGAGGTGTGTGAAGGCGATGAGGAGGACCTTACAGGCGCAACCCCATTTCTTCAACCGTCTAC 720
Qy 960 |||||ATCAGTGTCCGACTCTTAAAGATTCCAAACGATTTATCCAGGTGACCAAGTCTGGGCTC 1019
Db 721 |||||ATCAGTGTCCGACTCTTAAAGATTCCAAACGATTTATCCAGGTGACCAAGTCTGGGCTC 780
Qy 1020 |||||TTTCTGGCCCTCTGGGGATTACTTAAACAGAACTGGCAATGAGAAAGTCTCACTGCC 1079
Db 781 |||||TTTCTGGCCCTCTGGGGATTACTTAAACAGAACTGGCAATGAGAAAGTCTCACTGCC 840
Qy 1080 |||||TATCTGATTTACATGAGAACTGGGGATGCTGTGGGTGGGGGCCCACTTCCACAGAG 1139
Db 841 |||||TATCTGATTTACATGAGAACTGGGGATGCTGTGGGTGGGGGCCCACTTCCACAGAG 900
Qy 1140 |||||GAGCAATGACAGAGGTGCTGTGAGTTGAGATACAGCTGGCCCAATCAAGTGTCCAG 1199
Db 901 |||||GAGCAATGACAGAGGTGCTGTGAGTTGAGATACAGCTGGCCCAATCAAGTGTCCAG 960
Qy 1200 |||||GACCAAGGCGGACAGAGGAGATCTACCAAGATGAGCAATTCGGAGCTGCGAGGCT 1259
Db 961 |||||GACCAAGGCGGACAGAGGAGATCTACCAAGATGAGCAATTCGGAGCTGCGAGGCT 1020
Qy 1260 |||||CTGGCCGCTTCAATGACTGGCTGTGAGTTCTGTCTTCTTCTGTCTGCAACATTTGAGATTG 1319
Db 1021 |||||CTGGCCGCTTCAATGACTGGCTGTGAGTTCTGTCTTCTTCTGTCTGCAACATTTGAGATTG 1080
Qy 1320 |||||AGTGACTGTGAGCTGTGTGTGTATGAGATGATATTTTTCAGACAGGTGTGAGAGCTC 1379
Db 1081 |||||AGTGACTGTGAGCTGTGTGTGTATGAGATGATATTTTTCAGACAGGTGTGAGAGCTC 1140
Qy 1380 |||||ATCAACCGACCGAACAAGCATCTGAAATTAACCTGATCTGGAACTGGGCAAAAG 1439
Db 1141 |||||ATCAACCGACCGAACAAGCATCTGAAATTAACCTGATCTGGAACTGGGCAAAAG 1200
Qy 1440 |||||ACAACTCAAGCTGTGACCGACCTTGTGAGTCTGCAACAGAGAGCTGTGAGAGCTTC 1499
Db 1201 |||||ACAACTCAAGCTGTGACCGACCTTGTGAGTCTGCAACAGAGAGCTGTGAGAGCTTC 1260
Qy 1500 |||||TATGCACTTAAGAGTCTGTGTGCGAGGTGCGAGACTGTCTTCAACAGAGATGAC 1559
Db 1261 |||||TATGCACTTAAGAGTCTGTGTGCGAGGTGCGAGACTGTCTTCAACAGAGATGAC 1320
Qy 1560 |||||GCCCTTGGCTTCTTGGGGTCCCTTGTGTAAGGCGACGTTTGAACGGGCAAGGAA 1619
Db 1321 |||||GCCCTTGGCTTCTTGGGGTCCCTTGTGTAAGGCGACGTTTGAACGGGCAAGGAA 1380
Qy 1620 |||||GAAATTTGACAGAGGAGTATCAGCGAAATCCGACCGCATTTGAGAGGCGCTGGAGAG 1679
Db 1381 |||||GAAATTTGACAGAGGAGTATCAGCGAAATCCGACCGCATTTGAGAGGCGCTGGAGAG 1440
Qy 1680 |||||CTGGTTTGGATGATGAGAAAGACCCCGCAGGCGACCAAGAGAAAGCAGATGCTTAT 1739
Db 1441 |||||CTGGTTTGGATGATGAGAAAGACCCCGCAGGCGACCAAGAGAAAGCAGATGCTTAT 1500
Qy 1740 |||||GATATGATGTTTCCAGACTTATCTGTGAGCCCAAGAGGCTGATGATGTTTATGAC 1799
Db 1501 |||||GATATGATGTTTCCAGACTTATCTGTGAGCCCAAGAGGCTGATGATGTTTATGAC 1560
Qy 1800 |||||GGGTACGAAATTTCTGAGATCTTCTTCTTCCAAACAGTGTGAATTTGTACAACTTCTCT 1859
Db 1561 |||||GGGTACGAAATTTCTGAGATCTTCTTCTTCCAAACAGTGTGAATTTGTACAACTTCTCT 1620
Qy 1860 |||||GCCAAGTTATGCTGACACAGCTCCGCAAGCTTCCCAAGCTCCGAGACCAAGTGTGACATGAC 1919
Db 1621 |||||GCCAAGTTATGCTGACACAGCTCCGCAAGCTTCCCAAGCTCCGAGACCAAGTGTGACATGAC 1680
Qy 1920 |||||CCCCAGACAGTGAATGCTACTACCTTCCAACTTGAATGAGATGCTTCCCGGCTGGC 1979
Db 1681 |||||CCCCAGACAGTGAATGCTACTACCTTCCAACTTGAATGAGATGCTTCCCGGCTGGC 1740
Qy 1980 |||||ATCCTGACAGGCCCCCTTCTATATGCGCGCAACACCCCAAGGCTGTGAATCTTGGTGCATC 2039
Db 1741 |||||ATCCTGACAGGCCCCCTTCTATATGCGCGCAACACCCCAAGGCTGTGAATCTTGGTGCATC 1800
Qy 2040 |||||GGTGTGCTCATGGGCGCATGAGTTGACGATGCTTTGATGACCAAGGCGCGCATGATGAC 2099
Db 1801 |||||GGTGTGCTCATGGGCGCATGAGTTGACGATGCTTTGATGACCAAGGCGCGCATGATGAC 1860
Qy 2100 |||||AAGAGAGGGAACCTGGGCGCCCTGTGTGAGAAATGAGTCCCTGACGCTTCCGGAACAC 2159
Db 1861 |||||AAGAGAGGGAACCTGGGCGCCCTGTGTGAGAAATGAGTCCCTGACGCTTCCGGAACAC 1920
Qy 2160 |||||ACGGCTGTGATGAGGAAACAGTACATTAATCAATGATGAGGAGAGGCTCAACGCGC 2219
Db 1921 |||||ACGGCTGTGATGAGGAAACAGTACATTAATCAATGATGAGGAGAGGCTCAACGCGC 1980
Qy 2220 |||||CGCCAGACGCTGGGGGAGAAACATTTGCTGACAAAGGGGGCTGAAGCTGTGCTTCAATGCT 2279
Db 1981 |||||CGCCAGACGCTGGGGGAGAAACATTTGCTGACAAAGGGGGCTGAAGCTGTGCTTCAATGCT 2040
Qy 2280 |||||TACAAAGCATGGCTGAGAAAGCATGAGGAGAGACAACTGACAGCCGCGGAGCTCACG 2339
Db 2041 |||||TACAAAGCATGGCTGAGAAAGCATGAGGAGAGACAACTGACAGCCGCGGAGCTCACG 2100
Qy 2340 |||||AACCAACAGCTCTTCTTGTGTGAGTTTGGCCAGGTGTGTGCTCGGTCCGCAACAGAG 2399
Db 2101 |||||AACCAACAGCTCTTCTTGTGTGAGTTTGGCCAGGTGTGTGCTCGGTCCGCAACAGAG 2160
Qy 2400 |||||AGCTTCAAGAGGGGCTGTGTGACCGACCCCAAGCTTGTGCTTCCGCTGTGCGGCT 2459
Db 2161 |||||AGCTTCAAGAGGGGCTGTGTGACCGACCCCAAGCTTGTGCTTCCGCTGTGCGGCT 2220
Qy 2460 |||||ACTCTTCAACCTCCGCTGATCTTCCGCGGCACTTGGGCTGCGCTGCGCTCCGCTCCCATG 2519
Db 2221 |||||ACTCTTCAACCTCCGCTGATCTTCCGCGGCACTTGGGCTGCGCTGCGCTCCGCTCCCATG 2280
Qy 2520 |||||AACCCAGGACAGTGTGTGAGGTGTGTGAGCTGTGATCAGGAGGAGAAATGCCCCAGCTGT 2579
Db 2281 |||||AACCCAGGACAGTGTGTGAGGTGTGTGAGCTGTGATCAGGAGGAGAAATGCCCCAGCTGT 2240
Qy 2580 |||||CACCAAGCTGGGGACAGCTCTCTGTGACAAAGCTGTGCTTGTGGGTGTGGAGGAGCA 2639
Db 2341 |||||CACCAAGCTGGGGACAGCTCTCTGTGACAAAGCTGTGCTTGTGGGTGTGGAGGAGCA 2400
Qy 2640 |||||ATGCAAGCTGGGCTGGGCTGATGCTTCCGCGGCAAGGCTGACATGATGACAGACCTTC 2699
Db 2401 |||||ATGCAAGCTGGGCTGGGCTGATGCTTCCGCGGCAAGGCTGACATGATGACAGACCTTC 2460
Qy 2700 |||||TCAATCACCACATTTGTGCTGTGCTTGTGGGGGTGCGCTGTCCAGCAGAGCCGCCAC 2759
Db 2461 |||||TCAATCACCACATTTGTGCTGTGCTTGTGGGGGTGCGCTGTCCAGCAGAGCCGCCAC 2520
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QY 2760 ATTCACTGTAACATCTTCCGTGTCAACCCGCTGGAAGAGGTGTGGGTGGGAGGCCAG 2819  
DB 2521 ATTCACTGTAACATCTTCCGTGTCAACCCGCTGGAAGAGGTGTGGGTGGGAGGCCAG 2580  
QY 2820 TTCCCATAGGAAGAGCTGTCC 2841  
DB 2581 TTCCCATAGGAAGAGCTGTCC 2602

## RESULT 8

US-09-978-608A-525

Sequence 525, Application US/09978608A

Publication No. US20030045462A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C22  
CURRENT APPLICATION NUMBER: US/09/978,608A  
PRIORITY FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 525  
LENGTH: 2602  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-525

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2463; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCTGCTCTAGAGATGATGAGATTTCAGAGGGGCAAGAGAGCTGTAGGCTCAGC 419  
DB 121 CTGGAGAGCTGGAGCAAGTGGGATTTCAGAGGGGCAAGAGAGCTGTAGGCTCAGC 180  
QY 420 ACCGAGCTGAGAGCTGTCTTACAGAGGTCCTCTTACTGCTGTGAGTGTCTTGGG 479  
DB 181 ACCGAGCTGAGAGCTGTCTTACAGAGGTCCTCTTACTGCTGTGAGTGTCTTGGG 240  
QY 480 TGCTGTGAGCCATGAGGGTCCAGTACACAGAGACCATTCCACAGACCTGCTTACA 539  
DB 241 TGCTGTGAGCCATGAGGGTCCAGTACACAGAGACCATTCCACAGACCTGCTTACA 300  
QY 540 GAGGCTGATCTGAGTGTGAGAAATCTGTGAGTCCCTGAGCCGAGGGGTGAGCC 599

DB 301 GAGGCTGATCTGAGTGTGAGAAATCTGTGAGTCCCTGAGCCGAGGGGTGAGCC 360  
QY 600 TGTGAGAGATTTTACAGATTCTCTGTGGGGCTGAGATTGGAGAGACCCCTGCGCAT 659  
DB 361 TGTGAGAGATTTTACAGATTCTCTGTGGGGCTGAGATTGGAGAGACCCCTGCGCAT 420  
QY 660 GGGCGTTCTGCTGAGAACATCTTCAACAGCTCTGAGACCAAAACAGGCTACTGAG 719  
DB 421 GGGCGTTCTGCTGAGAACATCTTCAACAGCTCTGAGACCAAAACAGGCTACTGAG 480  
QY 720 CACCTGCTTGAACACCACTTCACTCCAGAGTGAAGTGTGAGCAAGACAGCC 779  
DB 481 CACCTGCTTGAACACCACTTCACTCCAGAGTGAAGTGTGAGCAAGACAGCC 540  
QY 780 TTCTACCTATCTTGCTTACAGGTGAGGAGCTTGAAGAGCTGGAGCCAGCACTGAG 839  
DB 541 TTCTACCTATCTTGCTTACAGGTGAGGAGCTTGAAGAGCTGGAGCCAGCACTGAG 600  
QY 840 GACCTCATTTGAGAGATTGTGTGTGGAATTAACGGGCTGTGGAGCAGAGCACTT 899  
DB 601 GACCTCATTTGAGAGATTGTGTGTGGAATTAACGGGCTGTGGAGCAGAGCACTT 660  
QY 900 ATGAGAGTGTGAGAGCACTGAGAGGAGCTTACAGGGCCACCCCATTTTCACTGAC 959  
DB 661 ATGAGAGTGTGAGAGCACTGAGAGGAGCTTACAGGGCCACCCCATTTTCACTGAC 720  
QY 960 ATCAGTCCGAGCTTGAAGTTCACAGCAATGTTATCAGGTGAGCAGTGTGGCTC 1019  
DB 721 ATCAGTCCGAGCTTGAAGTTCACAGCAATGTTATCAGGTGAGCAGTGTGGCTC 780  
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DB 781 TTTCTGCTCTGCGGATTTACTTAAACAGAACTGCCAATGAGAAAGTGTCTAC 840  
QY 1080 TATCTGATTAATGAGAGAACTGGGAGTGTCTGTGGGGGCGGCCCTTCCAGAG 1139  
DB 841 TATCTGATTAATGAGAGAACTGGGAGTGTCTGTGGGGGCGGCCCTTCCAGAG 900  
QY 1140 GAGCAGATGAGAGAGTGTGAGTGTGAGATGAGCTGGCCCAATCAAGTCCAG 1199  
DB 901 GAGCAGATGAGAGAGTGTGAGTGTGAGATGAGCTGGCCCAATCAAGTCCAG 960  
QY 1200 GACCAAGGCGGAGCAGAGAGAGATCTACCAAGATGAGATTTGAGAGTCCAGCT 1259  
DB 961 GACCAAGGCGGAGCAGAGAGAGATCTACCAAGATGAGATTTGAGAGTCCAGCT 1020  
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DB 1081 AGTGAATGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1140  
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DB 1141 ATCAACCGAGCAGAGCAAGCATCTGAACAATTAATCTGATCTGAACTGTGCAAA 1200  
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DB 1261 TATGAGCTAAGAGTCTGTGTGCGAGAGTGGCAGACCTGATCTCCAAACGATGAC 1320  
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DB 1321 GCCCTTGGCTTTGCTTTGGGGTCACTCTGTGAAGGCAAGTTTGAACCGCAAA 1380  
QY 1620 GAAATTTGAGAGGAGTGTATCAGCGAAATCCGAGCCGATTTGAGAGAGGCTGTGAG 1679  
DB 1381 GAAATTTGAGAGGAGTGTATCAGCGAAATCCGAGCCGATTTGAGAGAGGCTGTGAG 1440





QY 600 TGTGAGACCTTTACAGAGTTCTCTGTGGGGGCTGGAATTCGAGGAACCCCTGCCGAT 659  
DB 361 TGTGAGACCTTTACAGAGTTCTCTGTGGGGGCTGGAATTCGAGGAACCCCTGCCGAT 420  
QY 660 GGGCGTTCTCGTGAACAACCTTCAACAGCCTCTGGGACCAAAACAGGCCATATGAA 719  
DB 421 GGGCGTTCTCGTGAACAACCTTCAACAGCCTCTGGGACCAAAACAGGCCATATGAA 480  
QY 720 CACCTGCTGAAAAACACACCTTCAACTCCAGAGTGAAGCTGAGCAAGAACACAGCGC 779  
DB 481 CACCTGCTGAAAAACACACCTTCAACTCCAGAGTGAAGCTGAGCAAGAACACAGCGC 540  
QY 780 TTCTACTATCTTCCCTACAGGTGAGAGCGGATGAGAGGCTGGAGGCCGACCTGAG 839  
DB 541 TTCTACTATCTTCCCTACAGGTGAGAGCGGATGAGAGGCTGGAGGCCGACCTGAG 600  
QY 840 GACCTCATTTGAGAGATTTGGTGGTTGGAACTTACCGGGCCCTGGACACAGAACCTTT 899  
DB 601 GACCTCATTTGAGAGATTTGGTGGTTGGAACTTACCGGGCCCTGGACACAGAACCTTT 660  
QY 900 ATGAGAGTGTGAAGGAGTAGAGGAGCCTACAGGGCCACCCCATTTCTTCACTGCTAC 959  
DB 661 ATGAGAGTGTGAAGGAGTAGAGGAGCCTACAGGGCCACCCCATTTCTTCACTGCTAC 720  
QY 960 ATGAGAGTGTGAAGGAGTAGAGGAGCCTACAGGGCCACCCCATTTCTTCACTGCTAC 1019  
DB 721 ATGAGAGTGTGAAGGAGTAGAGGAGCCTACAGGGCCACCCCATTTCTTCACTGCTAC 780  
QY 1020 TTTCTGCGCTCTCGGGATTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
DB 781 TTTCTGCGCTCTCGGGATTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 840  
QY 1080 TATCTGATTAACATGAGAGAACTGGGGATCTGTGGTGGGGGCCCACTTCCAGAGG 1139  
DB 841 TATCTGATTAACATGAGAGAACTGGGGATCTGTGGTGGGGGCCCACTTCCAGAGG 900  
QY 1140 GACAGAGTGAAGAGGCTGAGAGTGAAGTACAGTGGCCAAATCAAGTGGCCAG 1199  
DB 901 GACAGAGTGAAGAGGCTGAGAGTGAAGTACAGTGGCCAAATCAAGTGGCCAG 960  
QY 1200 GACAGAGTGAAGAGGCTGAGAGTGAAGTACAGTGGCCAAATCAAGTGGCCAG 1259  
DB 961 GACAGAGTGAAGAGGCTGAGAGTGAAGTACAGTGGCCAAATCAAGTGGCCAG 1020  
QY 1260 CTGGCGCCCTTCATGAGCTGGCTTGAATCTGTCTTTCTTCTGTCAATTTGAGAGT 1319  
DB 1021 CTGGCGCCCTTCATGAGCTGGCTTGAATCTGTCTTTCTTCTGTCAATTTGAGAGT 1080  
QY 1320 AGTGAAGTGAAGCTGTGAGTGAAGTGAATTTGAGAGAGTGTGAGAGCTC 1379  
DB 1081 AGTGAAGTGAAGCTGTGAGTGAAGTGAATTTGAGAGAGTGTGAGAGCTC 1140  
QY 1380 ATCAACCGCAGGAGCCAGACATCTGAACTTGAATCTGAACTTGAATCTGAACTTGA 1439  
DB 1141 ATCAACCGCAGGAGCCAGACATCTGAACTTGAATCTGAACTTGAATCTGAACTTGA 1200  
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DB 1201 ACAAGCTCAAGCTTGAAGCCAGCTTGAATCTGCAAGAGAGTGTGAGAGCTC 1260  
QY 1500 TATGAGCACTAAGAGTCTGTGAGCGAGGAGGAGCCTGACATCTTCAACAGAGTAC 1559  
DB 1261 TATGAGCACTAAGAGTCTGTGAGCGAGGAGGAGCCTGACATCTTCAACAGAGTAC 1320  
QY 1560 GGCCTTGGCTTTGGGGTCCCTCTCTGTGAGGCGACGTTTGAACGCGCAAGCAAA 1619  
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QY 1620 GAAATTCAGAGGAGATGATCAGGAAATCCGACCGCATTTGAGGAGGCCCTGGAGCAG 1679  
DB 1381 GAAATTCAGAGGAGATGATCAGGAAATCCGACCGCATTTGAGGAGGCCCTGGAGCAG 1440

QY 1680 CTGTTTGGATGATGAGAGACCCGACGAGCCAAAGAGAAAGACAGATCCATCTAT 1739  
DB 1441 CTGTTTGGATGATGAGAGACCCGACGAGCCAAAGAGAAAGACAGATCCATCTAT 1500  
QY 1740 GATATGATTTGGTTTCCAGACTTTATCTGTGAGCCCAAAAGAGCTGATGATTTATGAC 1799  
DB 1501 GATATGATTTGGTTTCCAGACTTTATCTGTGAGCCCAAAAGAGCTGATGATTTATGAC 1560  
QY 1800 GGGTACGAAATTTTCGAGAAATCTTCTTCCAAAACATGTTGAATTTTGAACCTCTCT 1859  
DB 1561 GGGTACGAAATTTTCGAGAAATCTTCTTCCAAAACATGTTGAATTTTGAACCTCTCT 1620  
QY 1860 GCCAAGTATGAGCTGACAGAGCTCCGCAAGCTCCAGGCGAGACAGTGAAGTAC 1919  
DB 1621 GCCAAGTATGAGCTGACAGAGCTCCGCAAGCTCCAGGCGAGACAGTGAAGTAC 1680  
QY 1920 CCCAGACAGTGAATGCTTACTTACCTTCCAACTAAGATGAGTGTCTTCCCGCTGGC 1979  
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QY 1980 ATCTGAGAGCCCTCTTATGCGCGCAACACCCCAAGGCCCTGAACTTGGTGGCATC 2039  
DB 1741 ATCTGAGAGCCCTCTTATGCGCGCAACACCCCAAGGCCCTGAACTTGGTGGCATC 1800  
QY 2040 GGTGTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2099  
DB 1801 GGTGTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860  
QY 2100 AAAAGAGGAACTCTGCGGCCCTGTGTGAGAAATGAGTCCCTGAGCCTTCCGAAACAC 2159  
DB 1861 AAAAGAGGAACTCTGCGGCCCTGTGTGAGAAATGAGTCCCTGAGCCTTCCGAAACAC 1920  
QY 2160 AGGCGCTGATGAGAGGAAAGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2219  
DB 1921 AGGCGCTGATGAGAGGAAAGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1980  
QY 2220 CGCAGAGCTGTGGGAGAAATTTGCTGACAAAGGGGGCTGAAGGCTGCTCAATGCT 2279  
DB 1981 CGCAGAGCTGTGGGAGAAATTTGCTGACAAAGGGGGCTGAAGGCTGCTCAATGCT 2040  
QY 2280 TACAAAGCATGTGTAAGAAAGTGAAGGAGAGAGCACTGACAGCCTGTGGGCTCAC 2339  
DB 2041 TACAAAGCATGTGTAAGAAAGTGAAGGAGAGAGCACTGACAGCCTGTGGGCTCAC 2100  
QY 2340 AACCAAGCTCTTCTGTGGGAAATTTGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2399  
DB 2101 AACCAAGCTCTTCTGTGGGAAATTTGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2160  
QY 2400 AGCTCTCAAGAGGAGCTGTGAGCCAGCCCAAGCCTGCGCTTCCGCTGTGGGCT 2459  
DB 2161 AGCTCTCAAGAGGAGCTGTGAGCCAGCCCAAGCCTGCGCTTCCGCTGTGGGCT 2220  
QY 2460 ACTCTCTCAAGCTTCTGTGGGAAATTTGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2519  
DB 2221 ACTCTCTCAAGCTTCTGTGGGAAATTTGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2280  
QY 2520 AACCCAGGAGCTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2579  
DB 2281 AACCCAGGAGCTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2340  
QY 2580 CACCAAGCTGTGGGAGCTTCTCTGCAAAAGCTTGTCTTGTGGTTGGAGAGCA 2639  
DB 2341 CACCAAGCTGTGGGAGCTTCTCTGCAAAAGCTTGTCTTGTGGTTGGAGAGCA 2400  
QY 2640 ATGCAAGCTGTGGGCTGTAGTCTTCCCTCCCAAGTGTGACATGATGACAGACCTTCC 2699  
DB 2401 ATGCAAGCTGTGGGCTGTAGTCTTCCCTCCCAAGTGTGACATGATGACAGACCTTCC 2460  
QY 2700 TCAATCAACAAATTTGAGCTTGTGGGAGGAGCCCTGAGCTTCAAGAGAGCCCAAC 2759  
DB 2461 TCAATCAACAAATTTGAGCTTGTGGGAGGAGCCCTGAGCTTCAAGAGAGCCCAAC 2520  
QY 2760 ATTCACTGTGACATCTTCTCGTGTCACTGCTGTGAGAGAGTGTGGTGGGAGGCCAG 2819

Db 2521 ATTCACTGTGACATCTTCCGTGTCACTCCCTGGAGAGGCTCTGGTGGGAGGCGCAG 2580  
Qy 2820 TTCCCATAGGAGAGAGCTCTGCC 2841  
Db 2581 TTCCCATAGGAGAGAGCTCTGCC 2602

## RESULT 10

US-09-978-191A-525  
Sequence 525, Application US/09978191A  
Publication No. US2003050239A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austlin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978,191A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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;; PRIOR APPLICATION NUMBER: 60/085573  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2465; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCTGCTCTAGAGCTATGTTGGGATTCGAGAGGGGACAAAGACAGCTGTTAGGCTCAGCG 419  
DB 121 CTGGAGCTGGCAGCAAGTGGGATTCGAGAGGGGACAAAGACAGCTGTTAGGCTCAGCG 180

QY 420 ACGCAGCTGAGGTGCTTCTTAGCAGGTGCTCTACTGCTGAGCTGCACTGCTTGAGC 479  
DB 181 ACGCAGCTGAGGTGCTTCTTAGCAGGTGCTCTACTGCTGAGCTGCTGCTTGAGC 240  
QY 480 TGCCTTGTGGCCCTTAGGGGTCCAGTACCAAGAGACCCTCCACAGCAGCTGCTTACA 539  
DB 241 TGCCTTGTGGCCCTTAGGGGTCCAGTACCAAGAGACCCTCCACAGCAGCTGCTTACA 300  
QY 540 GAGGCTGCAATTCAGTGGCTGGAATAATCCCTGAGTCCCTGAGCCAGAGGGGTGAGCCCC 599  
DB 301 GAGGCTGCAATTCAGTGGCTGGAATAATCCCTGAGTCCCTGAGCCAGAGGGGTGAGCCCC 360  
QY 600 TGTGAGCAGCTTTTACCAAGTCTCTGTGGGGCTGGAATTCGAGAGAACCCCTGCCCCAT 659  
DB 361 TGTGAGCAGCTTTTACCAAGTCTCTGTGGGGCTGGAATTCGAGAGAACCCCTGCCCCAT 420  
QY 660 GGGCGTTCTCGCTGGAACAATTCAACAGCTCTGAGGACCAAAACAGGCCATTCAGAG 719  
DB 421 GGGCGTTCTCGCTGGAACAATTCAACAGCTCTGAGGACCAAAACAGGCCATTCAGAG 480  
QY 720 CACCTGCTTGAACCAACCACTTCAACCTCAGACAGTGAAGCTGAGAGAGACAGAGCCG 779  
DB 481 CACCTGCTTGAACCAACCACTTCAACCTCAGACAGTGAAGCTGAGAGAGACAGAGCCG 540  
QY 780 TTCTACCTATCTTGCCCTTACAGGTGAGCGCATTGAGAGAGCTGGAGCCAGCACTGAGA 839  
DB 541 TTCTACCTATCTTGCCCTTACAGGTGAGCGCATTGAGAGAGCTGGAGCCAGCACTGAGA 600  
QY 840 GACCTCATTTAGAGAGATGTTGGTTGGAACATTAACGGGCTCTGGAGCAAGAGCAACTTT 899  
DB 601 GACCTCATTTAGAGAGATGTTGGTTGGAACATTAACGGGCTCTGGAGCAAGAGCAACTTT 660  
QY 900 ATGAGAGTGTGAAGGCACTAGAGGAGCTTCAAGGAGCAACCCCATTTCTTCAACCTTAC 959  
DB 661 ATGAGAGTGTGAAGGCACTAGAGGAGCTTCAAGGAGCAACCCCATTTCTTCAACCTTAC 720  
QY 960 ATCAGTCCGACCTCTAAGAGTTCACACAGCAATGTTATCAGGTGAGCAAGTCTGGGCTC 1019  
DB 721 ATCAGTCCGACCTCTAAGAGTTCACACAGCAATGTTATCAGGTGAGCAAGTCTGGGCTC 780  
QY 1020 TTTCTGCCCTCTCGGGATTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
DB 781 TTTCTGCCCTCTCGGGATTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 840  
QY 1080 TATCTGATTTACATGAGAGAACTGGGGATGCTGCTGGGTGGGGGCCCACTCCAGAGG 1139  
DB 841 TATCTGATTTACATGAGAGAACTGGGGATGCTGCTGGGTGGGGGCCCACTCCAGAGG 900  
QY 1140 GAGCAGATGACAGAGGTGCTGAGTGTGAGATTAAGCTGGCCAACTCAAGTCCCCAG 1199  
DB 901 GAGCAGATGACAGAGGTGCTGAGTGTGAGATTAAGCTGGCCAACTCAAGTCCCCAG 960  
QY 1200 GACCAAGCGGCGGACGAGAGAGAAATCTACCAAGATGACATTTGAGACTGCAAGCTT 1259  
DB 961 GACCAAGCGGCGGACGAGAGAGAAATCTACCAAGATGACATTTGAGACTGCAAGCTT 1020  
QY 1260 CTGGGCGCTCCATGAGACTGCTTGGTCTCTCTCTTCTGCTGCAACATTTGAGATTG 1319  
DB 1021 CTGGGCGCTCCATGAGACTGCTTGGTCTCTCTCTTCTGCTGCAACATTTGAGATTG 1080  
QY 1320 AGTGACTTGAAGCTGTGAGTGTGATGAGATTAATTTGACAGAGGTGTCAGAGCTC 1379  
DB 1081 AGTGACTTGAAGCTGTGAGTGTGATGAGATTAATTTGACAGAGGTGTCAGAGCTC 1140  
QY 1380 ATCAACCGACGGAACCAAGCATCTGAAACAATTACTGATCTGGAACCTGCTGCAAAAG 1439  
DB 1141 ATCAACCGACGGAACCAAGCATCTGAAACAATTACTGATCTGGAACCTGCTGCAAAAG 1200  
QY 1440 ACAACCTCAAGCTGAGACCGACGCTTTGAGTCTGCAACAAGAGAGCTGCGAGACCTTC 1499  
DB 1201 ACAACCTCAAGCTGAGACCGACGCTTTGAGTCTGCAACAAGAGAGCTGCGAGACCTTC 1260  
QY 1500 TATGCACTTAAGAGTCTGTGTGCGAGGTGGCAAGCTGCATCTTCAACAGAGATGAC 1559



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7 PRIOR FILING DATE: 1998-03-20  
8 PRIOR APPLICATION NUMBER: 60/078936  
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11 PRIOR FILING DATE: 1998-03-20  
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133 PRIOR FILING DATE: 1998-05-15  
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141 PRIOR FILING DATE: 1998-05-15  
142 PRIOR APPLICATION NUMBER: 60/085573  
143 PRIOR FILING DATE: 1998-05-15  
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Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCGTCTAGAGCTATGAGGATTCAGAGAGGAGCAAGACAGCTGTTAGGCTCAGCG 419  
DB 121 CTGGAGCTGGCAGCAAGTGGGATTCAGAGAGGAGCAAGAGCTGTTAGGCTCAGCG 180  
QY 420 ACGACCTGAGAGCTGATCTTACAGAGTGCCTCTCTACCTGCTGCTGCTCTTCTGAGC 479  
DB 181 ACGACCTGAGAGCTGATCTTACAGAGTGCCTCTCTACCTGCTGCTGCTCTTCTGAGC 240  
QY 480 TGCCTTGTGGCCTTAGGGGTCCAGTACACAGAGACCCATCCACAGCACCTGCTTAC 539  
DB 241 TGCCTTGTGGCCTTAGGGGTCCAGTACACAGAGACCCATCCACAGCACCTGCTTAC 300  
QY 540 GAGGCTGATTCAGAGTGGCTGAGAAATCTGAGTCCCTGAGCCGAGGGGTGAGCCCG 599  
DB 301 GAGGCTGATTCAGAGTGGCTGAGAAATCTGAGTCCCTGAGCCGAGGGGTGAGCCCG 360  
QY 600 TGTGAGACTTTTACAGATTCCTCTGAGGGGCTGAGTTCAGAGAAACCCCTGAGCCGAT 659  
DB 361 TGTGAGACTTTTACAGATTCCTCTGAGGGGCTGAGTTCAGAGAAACCCCTGAGCCGAT 420  
QY 660 GGGCGTTCGCTGAGAAACCTTCAACAGCTCTGAGAACCAAGGCTATCTGAG 719  
DB 421 GGGCGTTCGCTGAGAAACCTTCAACAGCTCTGAGAACCAAGGCTATCTGAG 480  
QY 720 CACCTGCTGAGAAACCACTTCAACAGCTCTGAGAACCAAGGCTATCTGAG 779  
DB 481 CACCTGCTGAGAAACCACTTCAACAGCTCTGAGAACCAAGGCTATCTGAG 540  
QY 780 TTCTACCTATCTTCCCTACAGGTGAGCGCATTTGAGAGCTGAGAGCCCACTGAG 839  
DB 541 TTCTACCTATCTTCCCTACAGGTGAGCGCATTTGAGAGCTGAGAGCCCACTGAG 600  
QY 840 GACCTCATTTGAGAGATTTGGTGTGAAACATTAAGGGGCTGAGAACCACTT 899  
DB 601 GACCTCATTTGAGAGATTTGGTGTGAAACATTAAGGGGCTGAGAACCACTT 660  
QY 900 ATGAGAGTGTGAGAGCAGTACAGAGGAGCCTACAGGGGCAACCCATCTTCAACCGCTAC 959  
DB 661 ATGAGAGTGTGAGAGCAGTACAGAGGAGCCTACAGGGGCAACCCATCTTCAACCGCTAC 720  
QY 960 ATCAGTCCGAGCTCTAAGATTCACACAGCAATGTTATCAGGTGAGCAGTCTGAGCTC 1019  
DB 721 ATCAGTCCGAGCTCTAAGATTCACACAGCAATGTTATCAGGTGAGCAGTCTGAGCTC 780  
QY 1020 TTTCTGCTCTCTGAGATTACTTAACAAGACCTGCAATGAGAAAGTCTCACTGCTC 1079  
DB 781 TTTCTGCTCTCTGAGATTACTTAACAAGACCTGCAATGAGAAAGTCTCACTGCTC 840  
QY 1080 TATCTGAGATTAATGAGAGAACTGGGGAGTCTGCTGGGTGGGGGCTTCAAGAG 1139  
DB 841 TATCTGAGATTAATGAGAGAACTGGGGAGTCTGCTGGGTGGGGGCTTCAAGAG 900  
QY 1140 GAGCAGATCAGAGAGTCTGAGTGTGAGATTCAGCTGAGCAATCAAGTCCGAG 1199  
DB 901 GAGCAGATCAGAGAGTCTGAGTGTGAGATTCAGCTGAGCAATCAAGTCCGAG 960  
QY 1200 GACCAAGCGGCGAGCAGAGAGATCTACACAGATAGACATTTGAGAGTCAAGCT 1259  
DB 961 GACCAAGCGGCGAGCAGAGAGATCTACACAGATAGACATTTGAGAGTCAAGCT 1020  
QY 1260 CTGGGCGCTTCAATGAGCTGGCTTGGTCTCTTCTGCTGCTCACTTGGAGTGG 1319  
DB 1021 CTGGGCGCTTCAATGAGCTGGCTTGGTCTCTTCTGCTGCTCACTTGGAGTGG 1080  
QY 1320 AGTGACTTGAAGCTGTGTGTGTATGAGAGATTAATTTGAGCAGAGGTCTCAGAGCTC 1379

DB 1081 AGTGACTTGAAGCTGTGTGTGTATGAGAGATTAATTTGAGCAGAGGTCTCAGAGCTC 1140  
QY 1380 ATCAACCGGAGCGGAACCAAGCATCTCTGAACATTTACCTGATCTGAGAACTGGTGCAAG 1439  
DB 1141 ATCAACCGGAGCGGAACCAAGCATCTCTGAACATTTACCTGATCTGAGAACTGGTGCAAG 1200  
QY 1440 ACAACCTCAAGCCTGAGCCGAGCTTGTAGTCTGCAAGAGAGAGCTGTGAGACCTC 1499  
DB 1201 ACAACCTCAAGCCTGAGCCGAGCTTGTAGTCTGCAAGAGAGAGCTGTGAGACCTC 1260  
QY 1500 TATGCACTAAGAGTCTGTGTGCTGAGGTGAGAGCTGATCTCAACAGATGAC 1559  
DB 1261 TATGCACTAAGAGTCTGTGTGCTGAGGTGAGAGCTGATCTCAACAGATGAC 1320  
QY 1560 GCCCTTGGCTTGTGGGGTCCCTCTTCTGAGAGGCAAGTGTGACCGGCAAGCA 1619  
DB 1321 GCCCTTGGCTTGTGGGGTCCCTCTTCTGAGAGGCAAGTGTGACCGGCAAGCA 1380  
QY 1620 GAAATTCAGAGGGGATGATCAGCGAAATCCGGAACCGCATTTGAGAGGCTCTGGAGAG 1679  
DB 1381 GAAATTCAGAGGGGATGATCAGCGAAATCCGGAACCGCATTTGAGAGGCTCTGGAGAG 1440  
QY 1680 CTGTTTGGATGATGAGAGAGACCGGCAAGGAGCCAGAGAGAGAGATGATCTAT 1739  
DB 1441 CTGTTTGGATGATGAGAGAGACCGGCAAGGAGCCAGAGAGAGAGATGATCTAT 1500  
QY 1740 GATATGATTTGTTTCCAGACTTTATCTGTAGGCCCAAGAGCTGATGATTTATGAC 1799  
DB 1501 GATATGATTTGTTTCCAGACTTTATCTGTAGGCCCAAGAGCTGATGATTTATGAC 1560  
QY 1800 GGGTACGAAATTTTGAAGATCTTCTTCAAAACATGTGAAATTTGTACAACTCTCT 1859  
DB 1561 GGGTACGAAATTTTGAAGATCTTCTTCAAAACATGTGAAATTTGTACAACTCTCT 1620  
QY 1860 GCCAAGTTATGCTGACCAAGCTCCGCAAGCTCCAGCGGAGACCAAGTGAAGATGAC 1919  
DB 1621 GCCAAGTTATGCTGACCAAGCTCCGCAAGCTCCAGCGGAGACCAAGTGAAGATGAC 1680  
QY 1920 CCCGAGACGTGAATGCTTACTTCTTCAATGAATGAGATGCTTCCCGCTGGC 1979  
DB 1681 CCCGAGACGTGAATGCTTACTTCTTCAATGAATGAGATGCTTCCCGCTGGC 1740  
QY 1980 ATCCGAGAGGCCCTCTGATGCTCCGCAACCAAGGAGGCTGAACTCGGTGGATC 2039  
DB 1741 ATCCGAGAGGCCCTCTGATGCTCCGCAACCAAGGAGGCTGAACTCGGTGGATC 1800  
QY 2040 GGTGTGTCTATGAGGCAATGATTTGACGATGCTTGTGATGACCAAGGGGCGAGATGAC 2099  
DB 1801 GGTGTGTCTATGAGGCAATGATTTGACGATGCTTGTGATGACCAAGGGGCGAGATGAC 1860  
QY 2100 AAAAGAGGAACTCTGCGGCTCTGTGTGAGATGATCTTGGAGGCTTCCGAAACAC 2159  
DB 1861 AAAAGAGGAACTCTGCGGCTCTGTGTGAGATGATCTTGGAGGCTTCCGAAACAC 1920  
QY 2160 ACGGCTGATGAGAGAAACAGTAAATCAAGTCAAGGCTCAAGGGAGAGGCTCAACGGC 2219  
DB 1921 ACGGCTGATGAGAGAAACAGTAAATCAAGTCAAGGCTCAAGGGAGAGGCTCAACGGC 1980  
QY 2220 CGCAGAGCTGTGGGAGAACTTGTCTGCAACGAGGGGCTGAGAGCTCTCAATGCT 2279  
DB 1981 CGCAGAGCTGTGGGAGAACTTGTCTGCAACGAGGGGCTGAGAGCTCTCAATGCT 2040  
QY 2280 TACAAAGCATGGCTGAGAAAGCATGGGAGAGAGCAATGCTGAGCGGTGGGCTCAC 2339  
DB 2041 TACAAAGCATGGCTGAGAAAGCATGGGAGAGAGCAATGCTGAGCGGTGGGCTCAC 2100  
QY 2340 AACCAAGAGCTTCTTGTGTGAGATTTGCGCAAGGTGTGTGCTGCGACACAGAG 2399  
DB 2101 AACCAAGAGCTTCTTGTGTGAGATTTGCGCAAGGTGTGTGCTGCGACACAGAG 2160  
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DB 2161 AGCTCTCAAGAGGAGCTGTGACCGAGCCCAACAGCCCTGCTTCCGCTGTGAGG 2220





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PRIOR APPLICATION NUMBER:	60/085322
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15

[illegible]

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QY	1260	CTGGCGCCCTCCATGGAAGCTGGCTTGAAGTTCCTGTCTTTCTTGCTGTCAACATTTGGAAGTTG	1319
Db	1021	CTGGCGCCCTCCATGGAAGCTGGCTTGAAGTTCCTGTCTTTCTTGCTGTCAACATTTGGAAGTTG	1080
QY	1320	AGTGAATCTGAGCCCTGTGTGTGTGTATATGGAGATGATATATTTTGACAGAGTGTCAAGCTC	1379
Db	1081	AGTGAATCTGAGCCCTGTGTGTGTGTATATGGAGATGATATATTTTGACAGAGTGTCAAGCTC	1140
QY	1380	ATCAACCCGACCGGAACCAAGCATCTGTGAACATTTACCTGATCTGGAACTTGCTGTCAAAAG	1439
Db	1141	ATCAACCCGACCGGAACCAAGCATCTGTGAACATTTACCTGATCTGGAACTTGCTGTCAAAAG	1200
QY	1440	ACAACCTCAAGCTTGAGCCGAGCGCTTTGATGTGTGCAACAAGAGCTGCTGGAACCTC	1499
Db	1201	ACAACCTCAAGCTTGAGCCGAGCGCTTTGATGTGTGCAACAAGAGCTGCTGGAACCTC	1260
QY	1500	TATGGCACTAAGAAGTCCGTGTGTGCGAGGTGGAGACCTGCATCTCCAAACGGATGAC	1559
Db	1261	TATGGCACTAAGAAGTCCGTGTGTGCGAGGTGGAGACCTGCATCTCCAAACGGATGAC	1320
QY	1560	GCCCTTGGCTTTGCTTTGGGGTCCCTCTTCTGTGAAGGCAAGTTTGAACCGGCAAGCAAC	1619
Db	1321	GCCCTTGGCTTTGCTTTGGGGTCACTTCTTGTGAAGGCAAGTTTGAACCGGCAAGCAAC	1380
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Db	1381	GAAATTCGAGAGGGAGATGATCAGCGCAATTCGGAACCGCATTTGAGAGAGCCCTGGAGAG	1440
QY	1680	CTGTGTTGGATGATGAGAGAGACCCGCGAGGAGCGCAAGAGAAAGCATGTGCATCAT	1739
Db	1441	CTGTGTTGGATGATGAGAGAGACCCGCGAGGAGCGCAAGAGAAAGCATGTGCATCAT	1500
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Db	1501	GATATGATTTGGTTTCCCGACCTTATCTCGAGCCCAAGAGCTGAGATGATTATGAC	1560
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Db	1621	GCCAAAGTTATGCTGACCAAGCTCCGCAAGCCTCCAGCTGAGACCAATGAGATGAC	1680
QY	1920	CCCCGACAGTGAATGSCCTACTACTCTTCCACTAGATGAGATGATCTTCCCGCTGGC	1979
Db	1681	CCCCGACAGTGAATGSCCTACTACTCTTCCACTAGATGAGATGATCTTCCCGCTGGC	1740
QY	1980	ATCTCTGAGGCCCCCTTCTATGCCCCGCAACCACCCCAAGGCTCTGAATTCGTGTGACATC	2039
Db	1741	ATCTCTGAGGCCCCCTTCTATGCCCCGCAACCACCCCAAGGCTCTGAATTCGTGTGACATC	1800
QY	2040	GGTGTGTCTATGGCCCATGATGATTCGATGCGATGCTTTGATGATGACAAAGGCGCGAGTATGAC	2099
Db	1801	GGTGTGTCTATGGCCCATGATGATTCGATGCGATGCTTTGATGATGACAAAGGCGCGAGTATGAC	1860
QY	2100	AAAGAAAGGGAACCTGCGGGCCCTGTGTGGAGAGATGATGATCCCTGGGACGCTTCGGAAACAC	2159
Db	1861	AAAGAAAGGGAACCTGCGGGCCCTGTGTGGAGAGATGATGATCCCTGGGACGCTTCGGAAACAC	1920
QY	2160	ACGGCTCTGATGAGAGAACATGATCAATCAATACCAAGTCAAATGGGAGAGGCTCAACGGC	2219
Db	1921	ACGGCTCTGATGAGAGAACATGATCAATCAATACCAAGTCAAATGGGAGAGGCTCAACGGC	1980
QY	2220	CGCCAGAGCGCTGGGGGAGAACATTTGCTGACCAACGGGGGGCTGAGAGGCTGCTCAATATGCT	2279
Db	1981	CGCCAGAGCGCTGGGGGAGAACATTTGCTGACCAACGGGGGGCTGAGAGGCTGCTCAATATGCT	2040

OY	2280	TACAAAGCATGGCTGAGAAACATGGGAGGAGAGCACTGGCAGCGCTGGGCTCAC	2339
Db	2041	TACAAAGCATGGCTGAGAAACATGGGAGGAGAGCACTGGCAGCGCTGGGCTCAC	21000
OY	2340	AACCAACGACTCTTCTTCGTGGGATTGGCCACAGGTGTGTGCTCTGCACACAG	2399
Db	2101	AACCAACGACTCTTCTTCGTGGGATTGGCCACAGGTGTGTGCTCTGCACACAG	2160
OY	2400	AGCTTCCACGAGGGGCTGTGTACCCGACCCCAAGCCCTGGCCGCTTCCGGTGTGGG	2459
Db	2161	AGCTTCCACGAGGGGCTGTGTACCCGACCCCAAGCCCTGGCCGCTTCCGGTGTGGG	2220
OY	2460	ACTCTTCACAATCCCGGACCTTCCTGCGGCACTTCGGCTCCCTGTCCGCTCCCATG	2519
Db	2221	ACTCTTCCACAATCCCGGACCTTCCTGCGGCACTTCGGCTCCCTGTCCGCTCCCATG	2280
OY	2520	AACCCAGGCGAGCTGTGTGAGGTGTGTAGACTGTATCAGGGAGAAATGCCAGCTGT	2579
Db	2281	AACCCAGGCGAGCTGTGTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2340
OY	2580	CACCAAGACTGGGCGAGCTCTCTGTACAAGCTGTGTGTCTTGGGTTGGAGAGACAA	2639
Db	2341	CACCAAGACTGGGCGAGCTCTCTGTACAAGCTGTGTGTCTTGGGTTGGAGAGACAA	2400
OY	2640	ATGCAGTGGGGCTGGGTCTAGTCCCTCCCTCCCAAGGTGACATGTAGTAAAGACCTCC	2699
Db	2401	ATGCAGTGGGGCTGGGTCTAGTCCCTCCCTCCCAAGGTGACATGTAGTAAAGACCTCC	2460
OY	2700	TCAATTCACCAATTTGTGCTCTGTGCTTTGGGGGATGCCCTGCTCCAGACAGCCCAAC	2759
Db	2461	TCAATTCACCAATTTGTGCTCTGTGCTTTGGGGGATGCCCTGCTCCAGACAGCCCAAC	2520
OY	2760	ATTCACTGTGACATCTTTCCGCTGTACCCCTGTACCCCTGTGAGAGGTGTGGGTGGAGGCGAG	2819
Db	2521	ATTCACTGTGACATCTTTCCGCTGTACCCCTGTACCCCTGTGAGAGGTGTGGGTGGAGGCGAG	2580
OY	2820	TTCCCATGTGAGAGAGTCTGCC	2841
Db	2581	TTCCCATGTGAGAGAGTCTGCC	2602

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Sequence 525, Application US/0999833A  
Publication No. US20030054405A1  
GENERAL INFORMATION:  
APPLICANT: Ashtkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boctstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarolff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth U.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napiier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Pooni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630PIC65  
;; CURRENT APPLICATION NUMBER: US/09/999,833A  
;; CURRENT FILING DATE: 2001-10-24  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
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Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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181 ACCAGCTGAGCTGTCTTAGAGAGTCTCTCTACTGCTGCTGAGCTGTCTTGGGC 240  
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961 GACCAAGGCGGAG 1020  
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Db 2401 ATGCAAGCTGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
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Qy 2700 TCATCAACCAATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2759
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Db 2521 ATTCACTGTGACATCTTCCGTGTACCCCTGCGGAGAGGCTGTGGGTGGGAGGCGCAG 2580
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Qy 2820 TTCCCATAGGAGAGAGTCTGCC 2841
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RESULT 14
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; Sequence 525, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaerof, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
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34	PRIOR FILING DATE: 1998-05-15
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Query Match	72.9%;	Score 2461.2;	DB 10;	Length 2602;
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Db	121	CTGGAGAGCTGGACAGCAACGTGGGATTTCCAGAAAGGGGACAAACAGAGCTGTTATAGGCTACGC	180
QY	420	ACGACAGCTGAGAGCTGGTCTTTAGCAGAGTCCCTCTACTGTGTGCTGACACTGCTTTGGGC	479
Db	181	ACCGAGCTGGAGCTGGTCTTTAGCAGAGTCCCTCTACTGTGTGCTGACACTGCTTTGGGC	240
QY	480	TGCTCTGTGGCCCTTAGGGGTCCAGTACACAGAGACCCATCCCAACAGCACTGCTCTTACA	539
Db	241	TGCTCTGTGGCCCTTAGGGGTCCAGTACACAGAGACCCATCCCAACAGCACTGCTCTTACA	300
QY	540	GAGGCTGTGACTTGAAGTGGCTGAAAAAATCCTGAGTCCCTGACCCGAGGGGGTGAAGCCC	599
Db	301	GAGGCTGTGACTTGAAGTGGCTGAAAAAATCCTGAGTCCCTGACCCGAGGGGGTGAAGCCC	360
QY	600	TGTGAGGACTTTTATCCAGTTCCTCTGTGGGGGCTTGGATTCGGAGAAACCCCTGTCCCGAT	659
Db	361	TGTGAGGACTTTTATCCAGTTCCTCTGTGGGGGCTTGGATTCGGAGAAACCCCTGTCCCGAT	420
QY	660	GGGCGTTCTCGCTGGAACAACCTTCAACAGGCTCTTGGGACCAAAACAGAGCCATATGTAAG	719
Db	421	GGGCGTTCTCGCTGGAACAACCTTCAACAGGCTCTTGGGACCAAAACAGAGCCATATGTAAG	480
QY	720	CACCTGCTTGA AAAACACCACTTCAATTCACAGCAAGTAAAGCTGAGCGAAGACACAGCGC	779
Db	481	CACCTGCTTGA AAAACACCACTTCAATTCACAGCAAGTAAAGCTGAGCGAAGACACAGCGC	540
QY	780	TTTCACTCATCTTGCTGCTACAGGTGAGGCGCATTTGAGAGGCTGGGAGCCCACTGACACTGAGA	839
Db	541	TTTCACTCATCTTGCTGCTACAGGTGAGGCGCATTTGAGAGGCTGGGAGCCCACTGACACTGAGA	600
QY	840	GACCTCATTTGAGAAAGTTGGTGGTGAACAATTACGAGGGCCCTGGAGACACAGACACACTTT	899

Db 601 GACCTATTGAGAAAGTGGTGGTGGAACTTAACGGGGGCGCCGGAGCAGAGCAACTTT 660  
Qy 900 ATGAGAGTGTGAGAGCACTAGCAGAGCACTCAAGGCGCAACCCCATTTCTTACCGTCTAC 959  
Db 661 ATGAGAGTGTGAGAGCACTAGCAGAGCACTCAAGGCGCAACCCCATTTCTTACCGTCTAC 720  
Qy 960 ATCAGTGGCAGCTTAAGAGTTCCACAGCAATGTTATCCAGGTGAGCCAGTCTGGGCTC 1019  
Db 721 ATCAGTGGCAGCTTAAGAGTTCCACAGCAATGTTATCCAGGTGAGCCAGTCTGGGCTC 780  
Qy 1020 TTTCTGCGCTCTGGGATTACTACTTAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
Db 781 TTTCTGCGCTCTGGGATTACTACTTAACAGAACTGCCAATGAGAAAGTCTCACTGCC 840  
Qy 1080 TATCTGATTAATCAATGAGAACTGGGAGATGCTGGGGTGGGCGGCCCACTTCACAGAG 1139  
Db 841 TATCTGATTAATCAATGAGAACTGGGAGATGCTGGGGTGGGCGGCCCACTTCACAGAG 900  
Qy 1140 GAGCAGATGAGAGAGTGTGAGTGGAGATACAGTGGCCCAATCAAGTGGCCAG 1199  
Db 901 GAGCAGATGAGAGAGTGTGAGTGGAGATACAGTGGCCCAATCAAGTGGCCAG 960  
Qy 1200 GACCAAGGCGCGCAGAGAGAGATCTACCAAGATGAGCAATTCGAGCTGCAAGCT 1259  
Db 961 GACCAAGGCGCGCAGAGAGAGATCTACCAAGATGAGCAATTCGAGCTGCAAGCT 1020  
Qy 1260 CTGGCGCCCTCAATGAGCTGGTGAATTCCTGTCTTCTGTCTGCACTTGAAGTTG 1319  
Db 1021 CTGGCGCCCTCAATGAGCTGGTGAATTCCTGTCTTCTGTCTGCACTTGAAGTTG 1080  
Qy 1320 AGTGAATCTGAGAGCTGTGTGTGTGTATGGATGATTTATGAGCAGAGTGTCAAGCTC 1379  
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Qy 1380 ATCAACCGCAGCGAGCAAGCAATCTGAGCAATTAACCTGATCTGAGAACTGGTCAAAAG 1439  
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Qy 1440 ACAACCTCAAGCTTGAACCGACCTTGAATCTGCAACAAGAGAGCTGCTGAGAGCCCTC 1499  
Db 1201 ACAACCTCAAGCTTGAACCGACCTTGAATCTGCAACAAGAGAGCTGCTGAGAGCCCTC 1260  
Qy 1500 TATGCACTTAAGAAAGTCTGT 1559  
Db 1261 TATGCACTTAAGAAAGTCTGT 1320  
Qy 1560 GCCCTTGGCTTGT 1619  
Db 1321 GCCCTTGGCTTGT 1380  
Qy 1620 GAAATTTGAGAGAGAGTATCAGCGAAATCCGAGCCGATTTGAGAGAGCCCTGAGAGCAG 1679  
Db 1381 GAAATTTGAGAGAGAGTATCAGCGAAATCCGAGCCGATTTGAGAGAGCCCTGAGAGCAG 1440  
Qy 1680 CTGCTTTGATGATGAG 1739  
Db 1441 CTGCTTTGATGATGAG 1500  
Qy 1740 GATATGATTTGTTTCCAGACTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1799  
Db 1501 GATATGATTTGTTTCCAGACTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
Qy 1800 GGGTACGAAATTTCTGAGAGATTTCTTCTTCCAAACAGATTTGATTTGATCAACTTCTCT 1859  
Db 1561 GGGTACGAAATTTCTGAGAGATTTCTTCTTCCAAACAGATTTGATTTGATCAACTTCTCT 1620  
Qy 1860 GCCAAGTTATGCTGAG 1919  
Db 1621 GCCAAGTTATGCTGAG 1680  
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Db 1801 GGTGTGTATGAG 1860  
Qy 2100 AAAAG 2159  
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Qy 2160 ACAGCTGATGAG 2219  
Db 1921 ACAGCTGATGAG 1980  
Qy 2220 CGCAG 2279  
Db 1981 CGCAG 2040  
Qy 2280 TACAAAG 2339  
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Qy 2340 AACCAAG 2399  
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Qy 2400 AGCTGATGAG 2459  
Db 2161 AGCTGATGAG 2220  
Qy 2460 ACTCTCTCAACTCTCCGATGATCTCTGCGAGCACTTGAGCTGCTGCTGCTGCTGCTGCTGCT 2519  
Db 2221 ACTCTCTCAACTCTCCGATGATCTCTGCGAGCACTTGAGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Qy 2520 AACCAAG 2579  
Db 2281 AACCAAG 2340  
Qy 2580 CACCAAG 2639  
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Qy 2820 TTCCCATAG 2841  
Db 2581 TTCCCATAG 2602

RESULT 15  
US-09-978-824-525  
; Sequence 525, Application US/09978824  
; Publication No. US20030055216A1  
GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guirey, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Maly A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Qy	420	ACGCAAGCTGAGACTGTCTTAGCAGAGTGCCTCTTAATGCTGAGCTGCACTGTTCTGGGC	479	
Db	181	ACGCAAGCTGAGACTGTCTTAGCAGAGTGCCTCTTAATGCTGAGCTGCACTGTTCTGGGC	240	
Qy	480	TGCTTTGAGCCCTAGGGGTCAGATGACACAGAGACCATCCACAGACCTGACTTACA	539	
Db	241	TGCTTTGAGCCCTAGGGGTCAGATGACACAGAGACCATCCACAGACCTGACTTACA	300	
Qy	540	GAGGCTTGCAATTCGATGAGCTGAGAAAAATCTGTGAGTCCCTGAGACCGAGGGGTGAGCCCC	599	
Db	301	GAGGCTTGCAATTCGATGAGCTGAGAAAAATCTGTGAGTCCCTGAGACCGAGGGGTGAGCCCC	360	
Qy	600	TGTGAGGACTTTTACAGATTCTCTGTGAGGGGCTGAGATTGGAGGAAACCCCTGCGCGAT	659	
Db	361	TGTGAGGACTTTTACAGATTCTCTGTGAGGGGCTGAGATTGGAGGAAACCCCTGCGCGAT	420	
Qy	660	GAGGCTTCTCGTGGAGCACTTCAACAGCTCTTGAGAACAAACACAGGCCATTACTGAG	719	

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Db 1621 GCCAAGTTATGCTGACACGACTCCGCAAGCTTCCAGCCGAGACAGTGAACATGACC 1680  
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Db 1681 CCCGAGCAGTGAATGCTTACTACCTTCCACTAAGATGATGCTTCTTCCCGCTGAC 1740  
| | | | |  
QY 1980 ATCTGAGAGGCCCCCTTCTATGCCCCGCAACACCCCAAGGCCCTGAACTTGGTGGCAGTC 2039  
| | | | |  
Db 1741 ATCTGAGAGGCCCCCTTCTATGCCCCGCAACACCCCAAGGCCCTGAACTTGGTGGCAGTC 1800  
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QY 2040 GGTGTGTCATGAGGCGCATGATGACGATGCTTTGATGACCAAGGGCGGAGTATGAC 2099  
| | | | |  
Db 1801 GGTGTGTCATGAGGCGCATGATGACGATGCTTTGATGACCAAGGGCGGAGTATGAC 1860  
| | | | |  
QY 2100 AAAAAGAGAACTTGCAGCCCTGCTGAGAGATGATGCTTCTGCACTTCCGAAACAC 2159  
| | | | |  
Db 1861 AAAAAGAGAACTTGCAGCCCTGCTGAGAGATGATGCTTCTGCACTTCCGAAACAC 1920  
| | | | |  
QY 2160 ACGGCTGATGAGAGAAAGTACATCAATACAGGTCAATGAGGAGAGGCTCAACGAGC 2219  
| | | | |  
Db 1921 ACGGCTGATGAGAGAAAGTACATCAATACAGGTCAATGAGGAGAGGCTCAACGAGC 1980  
| | | | |  
QY 2220 CGCCAGACGCTGAGGAGAAATTTGCTGACAAACGAGGAGGCTGAAAGCTGCTCAATGCT 2279  
| | | | |  
Db 1981 CGCCAGACGCTGAGGAGAAATTTGCTGACAAACGAGGAGGCTGAAAGCTGCTCAATGCT 2040  
| | | | |  
QY 2280 TACAAAGCATGCTGAGAAAGCATGAGAGAGAGCACTGCCAGCCCTGAGGCTCAAC 2339  
| | | | |  
Db 2041 TACAAAGCATGCTGAGAAAGCATGAGAGAGAGCACTGCCAGCCCTGAGGCTCAAC 2100  
| | | | |  
QY 2340 AACCAACAGCTCTTCTGAGGAGTTGCCAGGTTGAGTGGTCCGACACACAG 2399  
| | | | |  
Db 2101 AACCAACAGCTCTTCTGAGGAGTTGCCAGGTTGAGTGGTCCGACACACAG 2160  
| | | | |  
QY 2400 AGCTCTCAGAGGAGGCTGATGACGACCCCAACAGCCCTGCTCCGCTGCTGGC 2459  
| | | | |  
Db 2161 AGCTCTCAGAGGAGGCTGATGACGACCCCAACAGCCCTGCTCCGCTGCTGGC 2220  
| | | | |  
QY 2460 ACTCTCTCAAACCTCCGTAATCTTCTGAGGCACTTGGGCTGCTGCTGCTCCCATG 2519  
| | | | |  
Db 2221 ACTCTCTCAAACCTCCGTAATCTTCTGAGGCACTTGGGCTGCTGCTGCTCCCATG 2280  
| | | | |  
QY 2520 AACCCAGGAGAGCTGATGAGTGTGATGACCTGATCAGGGAGAAATGCCAGCTGT 2579  
| | | | |  
Db 2281 AACCCAGGAGAGCTGATGAGTGTGATGACCTGATCAGGGAGAAATGCCAGCTGT 2340  
| | | | |  
QY 2580 CACCAGACTGAGGAGCACTCTCTGACAAAGCTTTGCTTTGGGTTGGAGAGAACAA 2639  
| | | | |  
Db 2341 CACCAGACTGAGGAGCACTCTCTGACAAAGCTTTGCTTTGGGTTGGAGAGAACAA 2400  
| | | | |  
QY 2640 ATGCAAGCTGAGGCTGAGTCTAGTCCCTCCCGCAAGTGAATGATACAGACCTTCC 2699  
| | | | |  
Db 2401 ATGCAAGCTGAGGCTGAGTCTAGTCCCTCCCGCAAGTGAATGATACAGACCTTCC 2460  
| | | | |  
QY 2700 TCAATGACCAATTTGCTCTGCTTGGGGGATGCCCTGCTCAGCAGAGCCCAACC 2759  
| | | | |  
Db 2461 TCAATGACCAATTTGCTCTGCTTGGGGGATGCCCTGCTCAGCAGAGCCCAACC 2520  
| | | | |  
QY 2760 ATTCACTGTGACATCTTCCGTGTCACTGCTGAAAGAGTCTGGGTGGAGGCGCAG 2819  
| | | | |  
Db 2521 ATTCACTGTGACATCTTCCGTGTCACTGCTGAAAGAGTCTGGGTGGAGGCGCAG 2580  
| | | | |  
QY 2820 TTCCCATAGGAAGAGTCTGCC 2841  
| | | | |  
Db 2581 TTCCCATAGGAAGAGTCTGCC 2602  
| | | | |

Search completed: July 3, 2004, 20:05:48  
Job time : 1396 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 16:34:27 ; Search time 74 Seconds  
(Without alignments)  
3096.568 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQLGLAGSNMVEYKRA.....RHFGCPVSPMNPGLCEW 811

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4281	100.0	811	6	ABG76487
2	3982.5	93.0	756	6	AAU92722
3	3824.5	89.3	736	2	AAI41774
4	3824.5	89.3	736	3	ABA44330
5	3824.5	89.3	736	4	AAU92233
6	3824.5	89.3	736	6	ABU58609
7	3824.5	89.3	736	6	ABU88157
8	3824.5	89.3	736	6	ABU84472
9	3824.5	89.3	736	6	ABR6346
10	3824.5	89.3	736	6	ABR65736
11	3824.5	89.3	736	6	ABU9676
12	3824.5	89.3	736	6	ABU82915
13	3824.5	89.3	736	6	ABU90036
14	3824.5	89.3	736	6	ABR68285
15	3824.5	89.3	736	6	ABU96338
16	3824.5	89.3	736	6	ABU92769
17	3824.5	89.3	736	6	ABO08846
18	3824.5	89.3	736	6	ABO02898
19	3824.5	89.3	736	6	ABR75052
20	3824.5	89.3	736	6	ABR94814
21	3824.5	89.3	736	6	ABO25276
22	3824.5	89.3	736	6	ABU85787
23	3824.5	89.3	736	6	ABU98947
24	3824.5	89.3	736	6	ABU98162
25	3824.5	89.3	736	6	ABU91868

26	3824.5	89.3	736	6	ABU72282	Abu72282 Novel hum
27	3824.5	89.3	736	6	ABU89561	Abu89561 Human PRO
28	3824.5	89.3	736	6	ABU86402	Abu86402 Human sec
29	3824.5	89.3	736	6	ABU67615	Abu67615 Human sec
30	3824.5	89.3	736	6	ABU80643	Abu80643 Human PRO
31	3824.5	89.3	736	6	ABR99561	Abu99561 Human sec
32	3824.5	89.3	736	6	ABR98951	Abu98951 Human sec
33	3824.5	89.3	736	6	ABO16474	Abu16474 Human sec
34	3824.5	89.3	736	6	ABR92374	Abu92374 Human sec
35	3824.5	89.3	736	6	ABO19015	Abu19015 Human sec
36	3824.5	89.3	736	6	ABR78436	Abu78436 Human sec
37	3824.5	89.3	736	6	ABO05172	Abu85172 Novel hum
38	3824.5	89.3	736	6	ABO00311	Abu00311 Novel hum
39	3824.5	89.3	736	6	ABO11643	Abu11643 Human sec
40	3824.5	89.3	736	6	ABO02288	Abu02288 Human sec
41	3824.5	89.3	736	6	ABU88862	Abu88862 Novel hum
42	3824.5	89.3	736	6	ABU83557	Abu83557 Human sec
43	3824.5	89.3	736	6	ABO06358	Abu06358 Novel hum
44	3824.5	89.3	736	6	ABR59394	Abu59394 Human sec
45	3824.5	89.3	736	6	ABO09456	Abu09456 Human sec

## ALIGNMENTS

RESULT 1  
ABG76487  
ID ABG76487 standard; protein; 811 AA.

AC ABG76487;  
DT 12-MAY-2003 (first entry)

DE Human zinc metalloprotease.  
XX

KW Human; enzyme; zinc metalloprotease; metastatic cancer; tumour;  
KW osteoarthritis; rheumatoid arthritis; septic arthritis;  
KW periodontal disease; corneal ulceration; proteinuria;  
KW coronary thrombosis; aneurysm aortic disease; birth control;  
KW dystrophic epidermolysis bullosa; degenerative cartilage loss;  
KW inflammatory response; osteopaenia; tempo mandibular joint disease;  
KW nervous system demyelinating disease; chromosome 3.

OS Homo sapiens.

PN US6482629-BI.

PD 19-NOV-2002.

PF 29-MAR-2001; 2001US-00819989.

PR 29-MAR-2001; 2001US-00819989.

PA (APPL-) APPLERA CORP.

PI Wei M, Yan C, Di Francesco V, Beasley EM;

DR WPI; 2003-298138/29.

DT N-PSDB; ABX13166, ABX13167.

PT New human zinc metalloprotease enzymes and nucleic acids encoding them,  
useful as models in developing and identifying human therapeutics, or as  
targets for developing therapeutic agents that modulate enzyme activity.

XX Claim 1; Fig 2; 49p; English.

CC The invention relates an isolated nucleic acid molecule (cDNA and gene)  
comprising a sequence encoding a human zinc metalloprotease. Also  
included are vectors and host cells for expression of the polypeptide.  
CC The human zinc metalloprotease and nucleic acids encoding them are useful  
as models in the development of human therapeutics, in the identification  
of therapeutic proteins, as targets for the development of human  
therapeutic agents that modulate enzyme activity in cells and tissues

CC expressing the enzyme, and as query sequences for sequence database  
CC searches for the identification of other family members or related  
CC sequences. The proteins may further be used to raise antibodies or to  
CC elicit another immune response, as a reagent in assays to quantitatively  
CC determine protein levels in biologic fluids, as markers for tissues in  
CC which the corresponding protein is expressed, as a target for diagnosing  
CC a disease or predisposition to a disease-mediated by the peptide, and for  
CC treating a disorder characterised by an absence or unwanted expression of  
CC the protein (e.g. metastatic cancer, tumour, osteoarthritis, rheumatoid  
CC arthritis, septic arthritis, periodontal disease, corneal ulceration,  
CC proteinuria, coronary thrombosis, aneurysm aortic disease, dystrophic  
CC epidermolysis bullosa, degenerative cartilage loss, inflammatory  
CC response, osteopaenia, tempero mandibular joint disease and nervous  
CC system demyelinating disease). The protein is also of use in birth  
CC control. The nucleic acids are useful as probes and primers, for  
CC constructing recombinant vectors, for monitoring effectiveness of  
CC modulating compounds on the expression or activity of the enzyme gene in  
CC clinical trials, and for constructing recombinant vectors. The gene for  
CC the metalloprotease is located on chromosome 3. The present sequence  
CC  
XX  
SQ Sequence 811 AA;  
Query Match 100.0%; Score 4281; DB 6; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNVALQELGAGSNMVEYKATLRDEDAPEPTVPGSGAPDMENYKSGAPSPSPGSGMP 60  
DB 1 MNVALQELGAGSNMVEYKATLRDEDAPEPTVPGSGAPDMENYKSGAPSPSPGSGMP 60  
QY 61 GTPRSSGLFMRVYCPHRSISGLCSRTMGVPOKGTROLLSRQLRLVLAGSLLAALL 120  
DB 61 GTPRSSGLFMRVYCPHRSISGLCSRTMGVPOKGTROLLSRQLRLVLAGSLLAALL 120  
QY 121 LGCLVALGVQYHRDPHSSTCLTEACIRVAKILLESIDRGVSPCEDFYFSGGMRNPL 180  
DB 121 LGCLVALGVQYHRDPHSSTCLTEACIRVAKILLESIDRGVSPCEDFYFSGGMRNPL 180  
QY 121 LGCLVALGVQYHRDPHSSTCLTEACIRVAKILLESIDRGVSPCEDFYFSGGMRNPL 180  
DB 121 LGCLVALGVQYHRDPHSSTCLTEACIRVAKILLESIDRGVSPCEDFYFSGGMRNPL 180  
QY 181 PDGRSRNTNSLMDQOAILKHLLENTTNSSEAEOKTORFLSCLQYERIEELGAP 240  
DB 181 PDGRSRNTNSLMDQOAILKHLLENTTNSSEAEOKTORFLSCLQYERIEELGAP 240  
QY 181 PDGRSRNTNSLMDQOAILKHLLENTTNSSEAEOKTORFLSCLQYERIEELGAP 240  
DB 181 PDGRSRNTNSLMDQOAILKHLLENTTNSSEAEOKTORFLSCLQYERIEELGAP 240  
QY 241 LRDLIEKIGGNITGPDODNFMEVLKAVAGTARATPFVYISADSKSNSNVIOVDS 300  
DB 241 LRDLIEKIGGNITGPDODNFMEVLKAVAGTARATPFVYISADSKSNSNVIOVDS 300  
QY 301 GLFLPSRDYILNRANKEKVLTAVIDYMEELGMLGGRPTSTREQMQLLELQLANITV 360  
DB 301 GLFLPSRDYILNRANKEKVLTAVIDYMEELGMLGGRPTSTREQMQLLELQLANITV 360  
QY 361 PODOREBEKTIYKMSISELQALAPSDMWEFLFSLSPLELSEPVVVYGMVDYQVDS 420  
DB 361 PODOREBEKTIYKMSISELQALAPSDMWEFLFSLSPLELSEPVVVYGMVDYQVDS 420  
QY 421 ELNRTSPSTILNNYILNLYOKTSSIDRRPESAOEKLTLVIGTKKSCVPMOTCSNT 480  
DB 421 ELNRTSPSTILNNYILNLYOKTSSIDRRPESAOEKLTLVIGTKKSCVPMOTCSNT 480  
QY 481 DDALGFALGSLFYKATFDROSKEIAEGMISEIRTAPEALGOLVMDDEKTRQAKEXADA 540  
DB 481 DDALGFALGSLFYKATFDROSKEIAEGMISEIRTAPEALGOLVMDDEKTRQAKEXADA 540  
QY 541 IYMWIGPPDPILEKELDVYDGEISEDSFQOMLNLNFSKAWADQKRPSPRQWS 600  
DB 541 IYMWIGPPDPILEKELDVYDGEISEDSFQOMLNLNFSKAWADQKRPSPRQWS 600  
QY 601 MTPQTVAAAYLPTKNEIVPAGILQAPFYARNPKALNFGIGVWGHETLTHAFDDQGR 660  
DB 601 MTPQTVAAAYLPTKNEIVPAGILQAPFYARNPKALNFGIGVWGHETLTHAFDDQGR 660  
QY 661 YDKEGNLRPMWQNESLAFRNHTACMEQYNOYVNGERLNGRQTLGENIADNGGLKAAAY 720  
DB 661 YDKEGNLRPMWQNESLAFRNHTACMEQYNOYVNGERLNGRQTLGENIADNGGLKAAAY 720

DB 661 YDKEGNLRPMWQNESLAFRNHTACMEQYNOYVNGERLNGRQTLGENIADNGGLKAAAY 720  
QY 721 NAYKALRKRGGEQQOIPANGLTNHOIFVGFPAQWCSVTPSPSSHGLVTPDHSPPRRV 780  
DB 721 NAYKALRKRGGEQQOIPANGLTNHOIFVGFPAQWCSVTPSPSSHGLVTPDHSPPRRV 780  
QY 781 LGTISNRDPLRHFGCPVSGPMNPQGLCEW 811  
DB 781 LGTISNRDPLRHFGCPVSGPMNPQGLCEW 811  
RESULT 2  
ID AAU82722 standard; protein; 766 AA.  
AC AAU82722;  
DT 23-APR-2002 (first entry)  
XX  
XX Amino acid sequence of novel human protease #21.  
XX  
XX Human; protease; cancer; immune-related disorder; cardiovascular disease;  
KW neuronal-associated disease; metabolic disorder; inflammatory disorder;  
KW nervous system disorder; sexual dysfunction; pain; mood disorder;  
KW hypertension; psychotic disorder; neurological disorder; dyskinesia;  
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;  
KW ocular disease; cytostatic; enzyme.  
XX  
XX Homo sapiens.  
OS  
PN MO200200860-A2.  
PD 03-JAN-2002.  
XX  
PF 26-JUN-2001; 2001WO-US020171.  
XX  
PR 26-JUN-2000; 2000US-0214047P.  
XX  
PA (SUGR-) SUGEN INC.  
XX  
PI Plozman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;  
PI Charyczak G;  
XX  
DR WPI; 2002-139913/18.  
DR N-PSDB; ABK31764.  
XX  
PT Nucleic acids encoding novel human proteases, useful for useful for  
PT treating diseases and disorders such as cancers, immune-related diseases  
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory  
PT disorders.  
XX  
PS Claim 6; Fig 21; 313pp; English.  
XX  
XX The present invention relates to the isolation of novel human proteases,  
CC and the nucleic acids encoding them. The sequences of the invention are  
CC useful for treating diseases and disorders such as cancers (e.g. breast,  
CC colon, lung), immune-related diseases and disorders (e.g. inflammatory  
CC diseases and asthma), cardiovascular diseases (e.g. restenosis and  
CC coronary thrombosis), brain or neuronal-associated diseases, metabolic  
CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.  
CC rheumatoid arthritis and psoriasis), central or peripheral nervous system  
CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention  
CC disorders, cognition disorders, hypotension, hypertension, psychotic  
CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's  
CC disease) and dyskinesias. The nucleic acids and polypeptides are also  
CC useful for treating viral infections caused by human immunodeficiency  
CC virus (HIV), and non-viral infections such as ocular disease (e.g.  
CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel  
CC human proteases of the invention  
XX  
SQ Sequence 766 AA;  
Query Match 93.0%; Score 3982.5; DB 5; Length 766;

Best Local Similarity 94.2%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 47; Gaps 2;

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QY 1 MNVALDELGAGNMVEYKATLTDEDAPEPTVEGASPDAMEYKAGASPPSPGSPQMT 60
Db 1 MNVALDELGAGNMVEYKATLTDEDAPEPTVEGASPDAME-----42
QY 61 GTRSSGLFWRVYCPHRSISGLCSRTMGPOKGTQLGSRQLDELVLGASILLAL 120
Db 43 -----VGFQKGTROLGSRQLDELVLGASILLAL 74
QY 121 LGLVALGVQYHNDPSHSTCLTEACIRVAKKILESIDRGVSPCEDFYQFCGGMIRNPL 180
Db 75 LGLVALGVQYHNDPSHSTCLTEACIRVAKKILESIDRGVSPCEDFYQFCGGMIRNPL 134
QY 181 PDGRSRMTFNSLMDONQAILKHLLENTTNSSEAEQKQRYFLSCLQYERIEIGACP 240
Db 135 PDGRSRMTFNSLMDONQAILKHLLENTTNSSEAEQKQRYFLSCLQYERIEIGACP 194
QY 241 LRDLIEKIGMNTTGPMDONFMEVLKAVGTRATPFFTVYISAKSSNSNVIOVDOS 300
Db 195 LRDLIEKIGMNTTGPMDONFMEVLKAVGTRATPFFTVYISAKSSNSNVIOVDOS 254
QY 301 GLFLPSRDYIANTANEKVLTAVIDYMEIGMLGGRPTSTRQMOQVLEIEIOLANITY 360
Db 255 GLFLPSRDYIANTANEKVLTAVIDYMEIGMLGGRPTSTRQMOQVLEIEIOLANITY 314
QY 361 PODQRDEEKIYHKMSISELOALAPSKMDIEFLSFLISPLESDSEPVVYVGMIDYLOQS 420
Db 315 PODQRDEEKIYHKMSISELOALAPSKMDIEFLSFLISPLESDSEPVVYVGMIDYLOQS 374
QY 421 ELINRTEPSILNNYILMNIYOKTSSIDRRFESAQOEKLETLGTKKSCVPRMOTCSNT 480
Db 375 ELINRTEPSILNNYILMNIYOKTSSIDRRFESAQOEKLETLGTKKSCVPRMOTCSNT 434
QY 481 DDALGALGSLFYKATFEDRSKEIAEG-MISEIRTAEEALGOLVMMDEKTRQAAKEXAD 539
Db 435 DDALGALGSLFYKATFEDRSKEIAEGMMSIERTAEBAALGOLVMMDEKTRQAAKEXAD 494
QY 540 AIYDMIGFDPFIIEPEKELDVYDGEI SEDSPFQNMMLNYSFAKWMADQLRKPPSHDQW 599
Db 495 AIYDMIGFDPFIIEPEKELDVYDGEI SEDSPFQNMMLNYSFAKWMADQLRKPPSHDQW 554
QY 600 SMTPOVNNAYYLPTKNEIVPPAGILOAFYARHHPKALNFGGIGVWGHETLTAFDQGR 659
Db 555 SMTPOVNNAYYLPTKNEIVPPAGILOAFYARHHPKALNFGGIGVWGHETLTAFDQGR 614
QY 660 EYDKENLRPMWONESIAFRNHTACMEEOYNOYQVNGERLNGRQTLGENIADNGGLKAA 719
Db 615 EYDKENLRPMWONESIAFRNHTACMEEOYNOYQVNGERLNGRQTLGENIADNGGLKAA 674
QY 720 YNAKAMLRHGEBOQLPAVGLTNHQLFPVGAQVMSVTPSSHEGLVTDHSPARFR 779
Db 675 YNAKAMLRHGEBOQLPAVGLTNHQLFPVGAQVMSVTPSSHEGLVTDHSPARFR 734
QY 780 VLGTLNSRDLRHHFGCPVSPMNPQQLCEW 811
Db 735 VLGTLNSRDLRHHFGCPVSPMNPQQLCEW 766
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RESULT 3  
AA41774  
ID AA41774 standard; protein; 736 AA.  
XX  
XX  
AC AA41774;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO403 protein sequence.  
XX  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.

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XX OS Homo sapiens.
XX PN W09946281-A2.
XX PD 16-SEP-1999.
XX PF 08-MAR-1999; 99WC-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 12-MAR-1998; 98US-0077649P.
XX 13-MAR-1998; 98US-0077791P.
XX 17-MAR-1998; 98US-0078004P.
XX 20-MAR-1998; 98US-0078042P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 26-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080105P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080157P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080127P.
XX 01-APR-1998; 98US-0080328P.
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XX 08-APR-1998; 98US-0081071P.
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XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082804P.
XX 23-APR-1998; 98US-0082767P.
XX 23-APR-1998; 98US-0082796P.
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XX 28-APR-1998; 98US-0083322P.
XX 28-APR-1998; 98US-0083392P.
XX 29-APR-1998; 98US-0083495P.
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XX 29-APR-1998; 98US-0083499P.
XX 29-APR-1998; 98US-0083500P.
XX 29-APR-1998; 98US-0083545P.
XX 29-APR-1998; 98US-0083554P.
XX 29-APR-1998; 98US-0083558P.
XX 29-APR-1998; 98US-0083559P.
XX 30-APR-1998; 98US-0083742P.
XX 05-MAY-1998; 98US-0084366P.
XX 06-MAY-1998; 98US-0084414P.
XX 06-MAY-1998; 98US-0084419P.
XX 07-MAY-1998; 98US-0084598P.
XX 07-MAY-1998; 98US-0084600P.
XX 07-MAY-1998; 98US-0084627P.
XX 07-MAY-1998; 98US-0084637P.
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PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085333P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
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PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086332P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
XX N-PSDB; AA234326.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 12; Fig 225; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AA233891 to AA234338, and AA241685 to
XX AA241774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 736 AA;
XX
XX Query Match 89.3%; Score 3824.5; DB 2; Length 736;
XX Best Local Similarity 99.9%; Pred. No. 1.2e-307;
XX Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 89 VGFQKGRQLGSTRTOLEVLGASLLALLLGCVLAVGVYHRDPSHSTCTBACIRY 148
XX 14 VGFQKGRQLGSTRTOLEVLGASLLALLLGCVLAVGVYHRDPSHSTCTBACIRY 73
XX
XX 149 AGILLESIDRGVSCEDFYQFSCGCGWIRRNPLPDGRSRMTFNSIMQONAILKHLENT 208
XX 74 AGILLESIDRGVSCEDFYQFSCGCGWIRRNPLPDGRSRMTFNSIMQONAILKHLENT 133
XX
XX 209 TFNSSSABEOKTORFYISCIQVERIEELGAQPLRDLIEKIGWNITGPMQDNFMETLKA 268
XX 134 TFNSSSABEOKTORFYISCIQVERIEELGAQPLRDLIEKIGWNITGPMQDNFMETLKA 193
XX
XX 269 VAGTYRATPEFTFYISDSKSSNSNVQOVOSGLFLPSRYLYNRTANEVLTAYLIDYME 338
XX 194 VAGTYRATPEFTFYISDSKSSNSNVQOVOSGLFLPSRYLYNRTANEVLTAYLIDYME 253
XX
XX 329 ELGMLLGRPTSTREQMQLVLELEIQLANITVTPQDRDEKITYHKMSISELQALAPSM 388
XX
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DB 254 ELGMLLGRPTSTREQMQLVLELEIQLANITVTPQDRDEKITYHKMSISELQALAPSM 313
QY 389 WLEFLSFLSPLELSSEPEVYVYGYNDYLOQVSELINRTPESTLNNYLTNNVQKTTSSLD 448
DB 314 WLEFLSFLSPLELSSEPEVYVYGYNDYLOQVSELINRTPESTLNNYLTNNVQKTTSSLD 373
QY 449 RRPESAQKLELTLYTKTKSCVPRMOTCISNTDDALGFALGSLFVATPDRSKETIAEGM 508
DB 374 RRPESAQKLELTLYTKTKSCVPRMOTCISNTDDALGFALGSLFVATPDRSKETIAEGM 433
QY 509 ISEIRTAPEEALGQLVWMDKTRQAKERADAIYDMIGPDFLEPKELDDVYDGEISE 568
DB 434 ISEIRTAPEEALGQLVWMDKTRQAKERADAIYDMIGPDFLEPKELDDVYDGEISE 493
QY 569 DSFFQNMNLNYPASAKVMDQLRKPPSRQMSMTQTVNAYYLPKNEIVPAGLIQAF 628
DB 494 DSFFQNMNLNYPASAKVMDQLRKPPSRQMSMTQTVNAYYLPKNEIVPAGLIQAF 553
QY 629 YARNHPKALNFGGIGVWGHBLTHAFDDQGREYDEKGNLRPMWNESLAFAFNHTACME 688
DB 554 YARNHPKALNFGGIGVWGHBLTHAFDDQGREYDEKGNLRPMWNESLAFAFNHTACME 613
QY 689 QYNQYVNGERLNGRQTIGENTADNGLKAAYNAYKAWLRKGEQQLPAVGLTNHQLFF 748
DB 614 QYNQYVNGERLNGRQTIGENTADNGLKAAYNAYKAWLRKGEQQLPAVGLTNHQLFF 673
QY 749 VGFQVWCGSVTRTPESHEGLVTDPHSPARFVLGTLTNSRDRLRHGCGVSGPMNPGQLC 808
DB 674 VGFQVWCGSVTRTPESHEGLVTDPHSPARFVLGTLTNSRDRLRHGCGVSGPMNPGQLC 733
QY 809 EYW 811
DB 734 EYW 736
XX
XX RESULT 4
XX ID AAB44330 standard; protein; 736 AA.
XX AC AAB44330;
XX DT 08-FEB-2001 (first entry)
XX XX
XX DE Human PRO403 protein sequence SEQ ID NO:526.
XX KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX expressed sequence tag; detection; cancer.
XX OS Homo sapiens.
XX PN WO200053756-A2.
XX PD 14-SEP-2000.
XX PF 18-FEB-2000; 2000WO-US004341.
XX
XX 08-MAR-1999; 99WO-US0005028.
XX 12-MAR-1999; 99US-0123857P.
XX 29-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
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PR 06-JAN-2000; 2000MO-US000376.  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,  
 PI Ferreira N, Filvaroff E, Fong S, Gao W, Geber H, Gerritsen ME,  
 PI Goddard A, Gidycz RJ, Grimaldi CJ, Gunney AL, Hillan KJ,  
 PI Kijavitt J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
 PI Stewart TA, Thomas D, Williams PM, Wood WI;  
 DR WPI; 2000-611443/58.  
 DR N-PSDB; AAC78592.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 XX  
 XX Claim 12; Fig 225; 636pp; English.  
 PS  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytosolic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences  
 CC  
 XX  
 XX Sequence 736 AA:  
 SO  
 Query Match 89.3%; Score 3824.5; DB 3; Length 736;  
 Best Local Similarity 99.9%; Pred. No. 1.2e-307;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 629 YARNHPRKALNFGSIGVYGMHGLTHAFDDQREYDKGNLRPMQNESLAAFRHTACME 688  
 DB 554 YARNHPRKALNFGSIGVYGMHGLTHAFDDQREYDKGNLRPMQNESLAAFRHTACME 613  
 QY 689 QYNQYVNGERLNGRQTIGENIADNGGLKAAVYAYAMLRKGEBOQLPAVGLTNHQLFF 748  
 DB 614 QYNQYVNGERLNGRQTIGENIADNGGLKAAVYAYAMLRKGEBOQLPAVGLTNHQLFF 673  
 QY 749 VGFPAQVWCVSRTPESSHEGLVTDPPHSPARPRVLTGTSNSRDLRHFQCPVGSPPMNTGQLC 808  
 DB 674 VGFPAQVWCVSRTPESSHEGLVTDPPHSPARPRVLTGTSNSRDLRHFQCPVGSPPMNTGQLC 733  
 QY 809 EVW 811  
 DB 734 EVW 736  
 RESULT 5  
 ID AAU29233 standard; protein; 736 AA.  
 AAU29233  
 AC AAU29233;  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #210.  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 OS Homo sapiens.  
 XX  
 PN MO200168848-A2.  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001MO-US006520.  
 XX  
 PR 01-MAR-2000; 2000MO-US0058601.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 06-MAR-2000; 2000US-0186968P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199554P.  
 PR 03-MAY-2000; 2000MO-US013705.  
 PR 17-MAY-2000; 2000MO-US014042.  
 PR 22-MAY-2000; 2000MO-US014941.  
 PR 30-MAY-2000; 2000MO-US015264.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.  
 PA  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2001-602746/68.  
 DR N-PSDB; AAS46134.  
 DR  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 XX Claim 11; Fig 420; 774pp; English.  
 PS  
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumor in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumor in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumor necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumors and also  
 CC susceptibility to tumor development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumors, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 XX Sequence 736 AA.  
 SO  
 Query Match 89.3%; Score 3824.5; DB 4; Length 736;  
 Best Local Similarity 99.9%; Pred. No. 1.2e-307;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 434 ISEIRTAFFBALGQLVMMDEKTRQAAKEKADAIYDMIGPDPFLPEKELDDVYDGEISE 493  
 QY 569 DSEFQMMALNLYNSACVADQIRKPPSSQMSMTPTQVNAVYLLPTNNEIVFPAIGLIQAF 628  
 DB 494 DSEFQMMALNLYNSACVADQIRKPPSSQMSMTPTQVNAVYLLPTNNEIVFPAIGLIQAF 553  
 QY 629 YARNHPKALNFGSIGVWVGHETLTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 688  
 DB 554 YARNHPKALNFGSIGVWVGHETLTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 613  
 QY 689 QYNQYVNGERLNGRQTIGENIADNGLKAAYNAVYKWLKXGEEQQLPAVGLTNHQLFF 748  
 DB 614 QYNQYVNGERLNGRQTIGENITDNGLKAAYNAVYKWLKXGEEQQLPAVGLTNHQLFF 673  
 QY 749 VGFPAQVCSVRTPESHHEGLVTDPHSPARFVLGTLNSRDPLRHFGCPVSGPMNGQLC 808  
 DB 674 VGFPAQVCSVRTPESHHEGLVTDPHSPARFVLGTLNSRDPLRHFGCPVSGPMNGQLC 733  
 QY 809 EYW 811  
 DB 734 EYW 736  
 RESULT 6  
 ID ABUS8609 standard; protein; 736 AA.  
 XX AC ABUS8609;  
 XX DT 15-APR-2003 (first entry)  
 XX DE Human PRO polypeptide #210.  
 XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;  
 XX antibody-dependent enzyme mediated prodrug therapy.  
 XX OS Homo sapiens.  
 XX UN US2003027272-A1.  
 XX PD 06-FEB-2003.  
 XX PE 21-JUN-2002; 2002US-00176492.  
 XX PF 18-SEP-1997; 97US-0059263P.  
 XX PR 18-SEP-1997; 97US-0059266P.  
 XX PR 17-OCT-1997; 97US-0062250P.  
 XX PR 21-OCT-1997; 97US-0063486P.  
 XX PR 24-OCT-1997; 97US-0063120P.  
 XX PR 24-OCT-1997; 97US-0063121P.  
 XX PR 28-OCT-1997; 97US-0063540P.  
 XX PR 28-OCT-1997; 97US-0063541P.  
 XX PR 28-OCT-1997; 97US-0063544P.  
 XX PR 28-OCT-1997; 97US-0063564P.  
 XX PR 29-OCT-1997; 97US-0063734P.  
 XX PR 31-OCT-1997; 97US-0063870P.  
 XX PR 31-OCT-1997; 97US-0064103P.  
 XX PR 31-OCT-1997; 97US-0065311P.  
 XX PR 13-NOV-1997; 97US-0065120P.  
 XX PR 21-NOV-1997; 97US-0066466P.  
 XX PR 24-NOV-1997; 97US-0066772P.  
 XX PR 11-DEC-1997; 97US-0069335P.  
 XX PR 12-DEC-1997; 97US-0069425P.  
 XX PR 17-DEC-1997; 97US-0069870P.  
 XX PR 18-DEC-1997; 97US-0068017P.  
 XX PR 10-MAR-1998; 98US-0077450P.  
 XX PR 11-MAR-1998; 98US-0077632P.  
 XX PR 11-MAR-1998; 98US-0077649P.  
 XX PR 20-MAR-1998; 98US-0078886P.  
 XX PR 20-MAR-1998; 98US-0078939P.  
 XX PR 27-MAR-1998; 98US-0079664P.



PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 01-APR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082588P.  
PR 21-APR-1998; 98US-0082589P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
PR 28-APR-1998; 98US-0083322P.  
PR 28-APR-1998; 98US-0083485P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083559P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086466P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 03-JUN-1998; 98US-0087759P.  
PR 04-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088366P.  
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PR 12-JUN-1998; 98US-0089105P.  
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PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
  
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PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
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PR 25-JUN-1998; 98US-0090696P.  
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PR 17-AUG-1998; 98US-0096891P.  
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PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0097022P.  
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PR 02-SEP-1998; 98US-0098843P.  
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PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099812P.  
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PR 16-SEP-1998; 98US-0101930P.  
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PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100843P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 23-SEP-1998; 98US-0101068P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101739P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101922P.  
PR 25-SEP-1998; 98US-0101922P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.

PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-00168978.

Query Match 89.3%; Score 3824.5; DB 6; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1,2e-307;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGRQLGSRTOELVLAGASILLALLGCVLVAQVYHRDPSHSTCLTEACIRV 148  
DB 14 VGFQKGRQLGSRTOELVLAGASILLALLGCVLVAQVYHRDPSHSTCLTEACIRV 73  
QY 149 AGKILSLDRGVSPCEDFYQPSCGWIRRNPLPDGRSMNTFNSLMDONAILKHILENT 208  
DB 74 AGKILSLDRGVSPCEDFYQPSCGWIRRNPLPDGRSMNTFNSLMDONAILKHILENT 133  
QY 209 TRNSSSAEOKTQRFYISCIQVERIEELGAPLDLIEKIGWNITGPMDQNFMEYLKA 268  
DB 134 TRNSSSAEOKTQRFYISCIQVERIEELGAPLDLIEKIGWNITGPMDQNFMEYLKA 193  
QY 269 VAGTYRATPFTFYISADSKSSNSNVTQVDSGLFLPSRDYLNRTANEKVLTRAYLDYME 328  
DB 194 VAGTYRATPFTFYISADSKSSNSNVTQVDSGLFLPSRDYLNRTANEKVLTRAYLDYME 253  
QY 329 ELGMLGGRPTSTREOMQVLELEIOLANITVPDQRDEDEKIYHKMSISELOALASMD 388  
DB 254 ELGMLGGRPTSTREOMQVLELEIOLANITVPDQRDEDEKIYHKMSISELOALASMD 313  
QY 389 WLEFLSLSLPLEISDESPVYVGMVLYQVSELIINTEPSILNNYILNMLVOKTSSLD 448  
DB 314 WLEFLSLSLPLEISDESPVYVGMVLYQVSELIINTEPSILNNYILNMLVOKTSSLD 373  
QY 449 RREPSAOKLELLETLYGFKSCVPRMOTCIENITDIALGALSLFKATFDRSKETIAEGM 508  
DB 374 RREPSAOKLELLETLYGFKSCVPRMOTCIENITDIALGALSLFKATFDRSKETIAEGM 433  
QY 509 ISEIRTAFFEBALGQVMMDEKTRQAAKEKADAIYDMIGPPDFILPEKELDDVDGYEISE 568  
DB 434 ISEIRTAFFEBALGQVMMDEKTRQAAKEKADAIYDMIGPPDFILPEKELDDVDGYEISE 493  
QY 569 DSFFQNNMLNYSFAKVMADQLRKRPSRDQSMTPQTVNAVYLPKNEIVFPAGILQAPF 628  
DB 494 DSFFQNNMLNYSFAKVMADQLRKRPSRDQSMTPQTVNAVYLPKNEIVFPAGILQAPF 553  
QY 629 YARNHPKALNFGGIGVVMGHELTAFDDQGREYDKENLRPMQNESIAAFRNHTACME 688  
DB 554 YARNHPKALNFGGIGVVMGHELTAFDDQGREYDKENLRPMQNESIAAFRNHTACME 613  
QY 689 QYNQYQVNGERLNGRQTLGENIADNGILKAAVNAVYKMLRKHGEEQQLPAVGLTNIQLFF 748  
DB 614 QYNQYQVNGERLNGRQTLGENIADNGILKAAVNAVYKMLRKHGEEQQLPAVGLTNIQLFF 673  
QY 749 VGFQKGRQLGSRTOELVLAGASILLALLGCVLVAQVYHRDPSHSTCLTEACIRV 808  
DB 674 VGFQKGRQLGSRTOELVLAGASILLALLGCVLVAQVYHRDPSHSTCLTEACIRV 733  
QY 809 EVW 811  
DB 734 EVW 736

RESULT 7  
ID ABU88157 standard; protein; 736 AA.  
AC ABU88157;  
XX  
DT 07-JUL-2003 (first entry)  
XX

DE Novel human secreted and transmembrane protein PRO740.

XX Human; secreted and transmembrane protein; PRO; gene therapy;  
KW tumour necrosis factor-alpha release; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

XX US2003032127-A1.

XX 13-FEB-2003.

XX 26-JUN-2002; 2002US-00183012.

XX 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 28-OCT-1997; 97US-0063121P.  
PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
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PR 31-OCT-1997; 97US-0064103P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 10-MAR-1998; 98US-007450P.  
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PR 20-MAR-1998; 98US-0078886P.  
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PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
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PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
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PR 09-APR-1998; 98US-0081195P.  
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PR 21-APR-1998; 98US-0082568P.  
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PR 07-MAY-1998; 98US-0084639P.  
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PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
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PR 10-JUN-1998; 98US-0088740P.  
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PR 19-JUN-1998; 98US-0089982P.  
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PR 22-JUN-1998; 98US-0090254P.  
PR 24-JUN-1998; 98US-0090429P.  
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PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
PR 01-JUL-1998; 98US-0091359P.  
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PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
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PR 24-JUL-1998; 98US-0094006P.  
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PR 18-AUG-1998; 98US-0096949P.  
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PR 18-AUG-1998; 98US-0097022P.

PR 26-AUG-1998; 98US-0097952P.  
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PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
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PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.

Query Match 89.3%; Score 3824.5; DB 6; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1,2e-307;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGTROLLGSRTOLEHVLGASILLALLLGCLVAGVOYHRDPSSHSTCTEACIRV 148  
DB 14 VGFQKGTROLLGSRTOLEHVLGASILLALLLGCLVAGVOYHRDPSSHSTCTEACIRV 73  
QY 149 AGKILESIDRGVSPCEDFYQPSGCGWIRRNPLPDGSRNMTNLSLMDONQAIKHLENT 208  
DB 74 AGKILESIDRGVSPCEDFYQPSGCGWIRRNPLPDGSRNMTNLSLMDONQAIKHLENT 133  
QY 209 TFFSSSEABOKTORFLYSLCLOVERIEELGAOPLRDILEKIGGNITGPMDDONFMEVLA 268  
DB 134 TFFSSSEABOKTORFLYSLCLOVERIEELGAOPLRDILEKIGGNITGPMDDONFMEVLA 193  
QY 269 VAGTYRATPEFTYVYISADSKSSNSNVIQVDSGLFLPSHDYVYLNRTANEKVLATAYDYNE 328  
DB 194 VAGTYRATPEFTYVYISADSKSSNSNVIQVDSGLFLPSHDYVYLNRTANEKVLATAYDYNE 253  
QY 329 ELGMLIGRPTSTREMOOVLBLEIOLANITTVPODORRDEKITYHMSISELOALAPSD 388  
DB 254 ELGMLIGRPTSTREMOOVLBLEIOLANITTVPODORRDEKITYHMSISELOALAPSD 313



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PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 25-JUN-1998; 98US-0090540P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090687P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
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PR 26-JUN-1998; 98US-0091010P.  
PR 01-JUL-1998; 98US-0091359P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
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PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091632P.  
PR 24-JUL-1998; 98US-0094006P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 10-AUG-1998; 98US-0095988P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 17-AUG-1998; 98US-0096757P.  
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PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-00168978.  
  
Query Match 89.3%; Score 3824.5; DB 6; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1,2e-107;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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DB 14 VGFQKGTROLLGSRTOLEVLVLAGASILLALLGLICLVALGVYHRDPHSSTCITEACIRV 73  
  
QY 149 AGKILSLRGVSPCSDPYOFGCGWIRRNPLPDGSRNNTFNSLMDONALIKHLENT 208  
DB 74 AGKILSLDRGVSPCSDPYOFGCGWIRRNPLPDGSRNNTFNSLMDONALIKHLENT 133  
  
QY 209 TFNSSSEAEOKTORFYLSCLQVERIELEGAOPLRDLIERIGWNITGPMDDNFMEVLA 268  
DB 134 TFNSSSEAEOKTORFYLSCLQVERIELEGAOPLRDLIERIGWNITGPMDDNFMEVLA 193  
  
QY 269 VAGTYRATPEFTYYSADSKSSNSNTIYVDOSGLFPLSPDYILNRPANEKVTATYIDYNE 328  
DB 194 VAGTYRATPEFTYYSADSKSSNSNTIYVDOSGLFPLSPDYILNRPANEKVTATYIDYNE 253  
  
QY 329 ELGMLIGRPSTRREMOOVLLEIOLANITVPODORRBEKIYHMSISELOALPSMD 388  
DB 254 ELGMLIGRPSTRREMOOVLLEIOLANITVPODORRBEKIYHMSISELOALPSMD 313  
  
QY 389 WLEFLSFLSLPLELSDBEPVVVYGM DYLOQVSELINRTEPSILNNYILNNLYOKTSSLD 448  
DB 314 WLEFLSFLSLPLELSDBEPVVVYGM DYLOQVSELINRTEPSILNNYILNNLYOKTSSLD 373  
  
QY 449 RRPESAQEKLETLVGTKKSCVPRMOTCISNTDDALGALGSLFVKATPDROSKETAEEM 508  
DB 374 RRPESAQEKLETLVGTKKSCVPRMOTCISNTDDALGALGSLFVKATPDROSKETAEEM 433  
  
QY 509 ISEIRTAFFREALGOLVMMDEKTRQAKERADAIYMIIGFPDFILKEKELDYYDGEIEIS 568  
DB 434 ISEIRTAFFREALGOLVMMDEKTRQAKERADAIYMIIGFPDFILKEKELDYYDGEIEIS 493  
  
QY 569 DSFFQNMNLNLYNSAKVMAVDOLRKPPSRDOMSMTPTVNAAYLLPTNGEIVFPAGIQAPF 628  
DB 494 DSFFQNMNLNLYNSAKVMAVDOLRKPPSRDOMSMTPTVNAAYLLPTNGEIVFPAGIQAPF 553  
  
QY 629 YARNHPKALNPGGIGVVMGHELTFAFDGGRDYDKGNLRPMWQNESLAFRNHTACMBE 688  
DB 554 YARNHPKALNPGGIGVVMGHELTFAFDGGRDYDKGNLRPMWQNESLAFRNHTACMBE 613  
  
QY 689 QYNQOVNGERLNGQOTGENTADNGGLKAAVNAAYAMRKKEGBOQLPAVGLTTHQLRF 748  
DB 614 QYNQOVNGERLNGQOTGENTADNGGLKAAVNAAYAMRKKEGBOQLPAVGLTTHQLRF 673  
  
QY 749 VGFPAQVWCVRTPPESHEGLVTDPSPARFRVLTGLTNSRDLTRHFGCPVGSPPMNGQLC 808  
DB 674 VGFPAQVWCVRTPPESHEGLVTDPSPARFRVLTGLTNSRDLTRHFGCPVGSPPMNGQLC 733  
  
QY 809 EYW 811  
DB 734 EYW 736

RESULT 9  
ID ABR66346 standard; protein; 736 AA.  
XX  
AC ABR66346;  
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DT 05-AUG-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO740, SEQ ID NO:420.  
XX  
XX Human; PRO; secreted protein; transmembrane protein;  
KM extracellular domain; tumor necrosis factor-alpha;  
KM chondrocyte; proliferation; differentiation; cartilage disorder;  
KM bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KM adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KM liver; drug screening; transgenic animal; genetic analysis;  
KM antiarthritic; vulnery; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027278-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176987.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
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QY 269 VAGTYRATPEFTYVISADSKSSNSNVIQVDSGLFLPSRDYILNRTANEKVLTAYLDMYE 328  
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XX antithrptic; vulnerary; gene therapy.  
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Best Local Similarity 99.9%; Pred. No. 1.2e-307;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 11
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DT 09-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX
PN US2003040070-A1.
XX
PD 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
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QY 149 AGKILSLDRGVSPCDPFOFSGCGWIRRNPLPDGSRNNNTNSLMDQOAILKHELENT 208  
DB 74 AGKILSLDRGVSPCDPFOFSGCGWIRRNPLPDGSRNNNTNSLMDQOAILKHELENT 133  
QY 209 TFNSSFSEAEQKTRFYLSCLQVERIBELGAQPLRDLIEKIGGNITGPMDOONFMEVLA 268  
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DT 11-AUG-2003 (first entry)  
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KW Human; Gene therapy; tissue typing; tumour; chondrocyte proliferation;  
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PD 20-FEB-2003.  
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 AC ABR68285;  
 DT 11-AUG-2003 (first entry)  
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 KW Human; PRO; secreted protein; transmembrane protein;  
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 KW chondrocyte; proliferation; differentiation; cartilage disorder;

KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antirheumatic; vulnery; gene therapy.  
OS Homo sapiens.  
PN US2003027264-A1.  
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PD 06-FEB-2003.  
PF 18-JUN-2002; 2002US-00174579.  
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QY	1	MNAVALGELGSGNMVEYKRA	1	100.0%	Score 4281; DB 4; Length 811;				
DB	1	MNAVALGELGSGNMVEYKRA	1	100.0%	Score 4281; DB 4; Length 811;				
QY	61	GTPRSSGLFWRYTCPLKRSISGLCSRTWVGFOKGTQQLGSRQLVLAAGSLLAALL	120						
DB	61	GTPRSSGLFWRYTCPLKRSISGLCSRTWVGFOKGTQQLGSRQLVLAAGSLLAALL	120						
QY	121	LGGLVAVGYVRHDSHSTCLTEACIRVAGKLTLESIDRGVSPCEDPYOPSCGGMIRNPL	180						
DB	121	LGGLVAVGYVRHDSHSTCLTEACIRVAGKLTLESIDRGVSPCEDPYOPSCGGMIRNPL	180						
QY	181	PDGRSMNTPNSLMDONQAILKHLLENTTFNSSSEAEOKTORYLSCLOVERIEELGAOP	240						
DB	181	PDGRSMNTPNSLMDONQAILKHLLENTTFNSSSEAEOKTORYLSCLOVERIEELGAOP	240						
QY	241	LRLDLIKIGGWNITGWDONFMEVLKAVAGYRATPFTVYISADSKSNSNVIOVDOS	300						
DB	241	LRLDLIKIGGWNITGWDONFMEVLKAVAGYRATPFTVYISADSKSNSNVIOVDOS	300						
QY	301	GLFLPSRDYLYNRTANEKYLTAIVDMEELGMLGSPSTREBOMQOVLLETOLANITY	360						
DB	301	GLFLPSRDYLYNRTANEKYLTAIVDMEELGMLGSPSTREBOMQOVLLETOLANITY	360						
QY	361	PODORDEEKIYHKMSISELOALAPSMDWLEFLSLPLELSDSEPVVYVGMVLYQOVS	420						
DB	361	PODORDEEKIYHKMSISELOALAPSMDWLEFLSLPLELSDSEPVVYVGMVLYQOVS	420						

Db 361 POPQRDEEKIYHKMSISELQALAPSMDWLEFLSLPLELSDSEPVVYVGYMDYLOQVS 420  
Qy 421 ELINRTEPSILNNYILNVLVOKTSSSLDRPESAOEKLTLVGTREKSCVPRMOTCISNT 480  
Db 421 ELINRTEPSILNNYILNVLVOKTSSSLDRPESAOEKLTLVGTREKSCVPRMOTCISNT 480  
Qy 481 DDALGFALGSLFVYKATFDROSKEIAEGMISEIRTAPEEALGOLVMMDEKTRQAAKEKADA 540  
Db 481 DDALGFALGSLFVYKATFDROSKEIAEGMISEIRTAPEEALGOLVMMDEKTRQAAKEKADA 540  
Qy 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSRDQWS 600  
Db 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSRDQWS 600  
Qy 601 MTPQTVNAYYLLPTKNEIVFPAGILQAPFYARHHPKALNFGGIGVWGHETLTHAFDDQGRE 660  
Db 601 MTPQTVNAYYLLPTKNEIVFPAGILQAPFYARHHPKALNFGGIGVWGHETLTHAFDDQGRE 660  
Qy 661 YDEKGNLRPMWQNESLAAFRNHTACMEEOYNOYVNGEELNQRQTLENTADNGGLKAAV 720  
Db 661 YDEKGNLRPMWQNESLAAFRNHTACMEEOYNOYVNGEELNQRQTLENTADNGGLKAAV 720  
Qy 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPHSPARFRV 780  
Db 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPHSPARFRV 780  
Qy 781 LGTLSNSRDPLRHFGCPVGSPPMNGQLCEW 811  
Db 781 LGTLSNSRDPLRHFGCPVGSPPMNGQLCEW 811

## RESULT 2

US-10-273-992-2  
; Sequence 2, Application US/10273992

; Patent No. 6664093  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001200D1V  
; CURRENT APPLICATION NUMBER: US/10/273,992  
; CURRENT FILING DATE: 2002-10-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 811  
; TYPE: PR1  
; ORGANISM: Human  
US-10-273-992-2

Query Match 100.0%; Score 4281; DB 4; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGGASPDAMEYVGKASPPSPGSPGMP 60  
Db 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGGASPDAMEYVGKASPPSPGSPGMP 60  
Qy 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWVGFQKGTROLLGSRTOLELVLAGASILLALL 120  
Db 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWVGFQKGTROLLGSRTOLELVLAGASILLALL 120  
Qy 121 LGCIVAGVOYHRDPHSSTCLTEACIRVAGKILLESIDRGVSPCEDFQFSGCGMIRNPL 180  
Db 121 LGCIVAGVOYHRDPHSSTCLTEACIRVAGKILLESIDRGVSPCEDFQFSGCGMIRNPL 180  
Qy 181 PDGSRKNTFNSLMDQOAILIKHLENTFNSSSEAROKTORFVLSGLQVERIEEAGAP 240  
Db 181 PDGSRKNTFNSLMDQOAILIKHLENTFNSSSEAROKTORFVLSGLQVERIEEAGAP 240  
Qy 241 LRDLIEKIGGWNITGPMQDQNFMEVLKAVAGYRATPFVTVYISADSKSNSNVYQVDS 300  
Db 241 LRDLIEKIGGWNITGPMQDQNFMEVLKAVAGYRATPFVTVYISADSKSNSNVYQVDS 300

Db 241 LRDLIEKIGGWNITGPMQDQNFMEVLKAVAGYRATPFVTVYISADSKSNSNVYQVDS 300  
Qy 301 GFLPSRDYVYLNNTAEKYLATADYMEELMGLGRPSTBROMQOVLELEIQLANITV 360  
Db 301 GFLPSRDYVYLNNTAEKYLATADYMEELMGLGRPSTBROMQOVLELEIQLANITV 360  
Qy 361 POPQRDEEKIYHKMSISELQALAPSMDWLEFLSLPLELSDSEPVVYVGYMDYLOQVS 420  
Db 361 POPQRDEEKIYHKMSISELQALAPSMDWLEFLSLPLELSDSEPVVYVGYMDYLOQVS 420  
Qy 421 ELINRTEPSILNNYILNVLVOKTSSSLDRPESAOEKLTLVGTREKSCVPRMOTCISNT 480  
Db 421 ELINRTEPSILNNYILNVLVOKTSSSLDRPESAOEKLTLVGTREKSCVPRMOTCISNT 480  
Qy 481 DDALGFALGSLFVYKATFDROSKEIAEGMISEIRTAPEEALGOLVMMDEKTRQAAKEKADA 540  
Db 481 DDALGFALGSLFVYKATFDROSKEIAEGMISEIRTAPEEALGOLVMMDEKTRQAAKEKADA 540  
Qy 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSRDQWS 600  
Db 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSRDQWS 600  
Qy 601 MTPQTVNAYYLLPTKNEIVFPAGILQAPFYARHHPKALNFGGIGVWGHETLTHAFDDQGRE 660  
Db 601 MTPQTVNAYYLLPTKNEIVFPAGILQAPFYARHHPKALNFGGIGVWGHETLTHAFDDQGRE 660  
Qy 661 YDEKGNLRPMWQNESLAAFRNHTACMEEOYNOYVNGEELNQRQTLENTADNGGLKAAV 720  
Db 661 YDEKGNLRPMWQNESLAAFRNHTACMEEOYNOYVNGEELNQRQTLENTADNGGLKAAV 720  
Qy 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPHSPARFRV 780  
Db 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPHSPARFRV 780  
Qy 781 LGTLSNSRDPLRHFGCPVGSPPMNGQLCEW 811  
Db 781 LGTLSNSRDPLRHFGCPVGSPPMNGQLCEW 811

## RESULT 3

US-09-819-989-4  
; Sequence 4, Application US/09819989

; Patent No. 6482629  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001200  
; CURRENT APPLICATION NUMBER: US/09/819,989  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 765  
; TYPE: PR1  
; ORGANISM: Human  
US-09-819-989-4

Query Match 93.3%; Score 3993; DB 4; Length 765;  
Best Local Similarity 94.3%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;  
Qy 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGGASPDAMEYVGKASPPSPGSPGMP 60  
Db 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGGASPDAMEYVGKASPPSPGSPGMP 60  
Qy 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWVGFQKGTROLLGSRTOLELVLAGASILLALL 120  
Db 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWVGFQKGTROLLGSRTOLELVLAGASILLALL 120  
Qy 121 LGCIVAGVOYHRDPHSSTCLTEACIRVAGKILLESIDRGVSPCEDFQFSGCGMIRNPL 180  
Db 121 LGCIVAGVOYHRDPHSSTCLTEACIRVAGKILLESIDRGVSPCEDFQFSGCGMIRNPL 180

Db 75 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 134  
QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORFYLSCLQVERIEELGAOP 240  
Db 135 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORFYLSCLQVERIEELGAOP 194  
QY 241 LRDLIEKIGGMNITGPMDDNFMFVILKAVAGTRATPFTVYISADSKSNSNVIOVDOS 300  
Db 195 LRDLIEKIGGMNITGPMDDNFMFVILKAVAGTRATPFTVYISADSKSNSNVIOVDOS 254  
QY 301 GLFLPSRDYILNRTANEKVLTAVIDYMEELGMLGGRPTSTREMOQVLELEIQLANITY 360  
Db 255 GLFLPSRDYILNRTANEKVLTAVIDYMEELGMLGGRPTSTREMOQVLELEIQLANITY 314  
QY 361 PDGRDEEKIYHKMSISELOALAPSDMWLEFLSLSPLEISDSSEPVVYVGMVDYLOQVS 420  
Db 315 PDGRDEEKIYHKMSISELOALAPSDMWLEFLSLSPLEISDSSEPVVYVGMVDYLOQVS 374  
QY 421 ELINRTEPSILNNYLIMNLVOKTSSLDRRFESAOKLETLTYGTKKSCVPRMOTCISNT 480  
Db 375 ELINRTEPSILNNYLIMNLVOKTSSLDRRFESAOKLETLTYGTKKSCVPRMOTCISNT 434  
QY 481 DDALGFALGSLFYKATFDROSKEIABGMISEIRTAFEALGOLVWMDKTRQAKAKADA 540  
Db 435 DDALGFALGSLFYKATFDROSKEIABGMISEIRTAFEALGOLVWMDKTRQAKAKADA 494  
QY 541 IYMGIPDFILPEKELDVIDYGEISEDSFQOMNLNLYNFSKAVADOLRKPSRDOS 600  
Db 495 IYMGIPDFILPEKELDVIDYGEISEDSFQOMNLNLYNFSKAVADOLRKPSRDOS 554  
QY 601 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARNHPKALNFGGIGVWNGHELTHAFDQGRE 660  
Db 555 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARNHPKALNFGGIGVWNGHELTHAFDQGRE 614  
QY 661 YDKEGMLRPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGJLKAAY 720  
Db 615 YDKEGMLRPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGJLKAAY 674  
QY 721 NAKAWLARKHGEEQQLPAVGLTNHQLFPVGFQAVWCVRTPSSHGLVTDPHSPARFRV 780  
Db 675 NAKAWLARKHGEEQQLPAVGLTNHQLFPVGFQAVWCVRTPSSHGLVTDPHSPARFRV 734  
QY 781 LGTILNSRDLRHFQCGVSPMNPQOLCEW 811  
Db 735 LGTILNSRDLRHFQCGVSPMNPQOLCEW 765

RESULT 4  
US-10-273-992-4  
; Sequence 4, Application US/10273992  
; Patent No. 6664093  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; FILE REFERENCE: CLO01200DIV  
; CURRENT APPLICATION NUMBER: US/10/273,992  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Human  
US-10-273-992-4

Query Match 93.3%; Score 3993; DB 4; Length 765;  
Best Local Similarity 94.3%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;  
1 MNVALQELGAGSNMVEYKRALTRDEDAPEPTVEGASPDAMEVGKASPPSPSPQMT 60

Db 1 MNVALQELGAGSNMVEYKRALTRDEDAPEPTVEGASPDAME----- 42  
QY 61 GTPRSSGLFMRVYTCPLRLASISGLCSRTWVGFOKQTRQLGSRTOLEVLVAGASILLALL 120  
Db 43 -----VFQGRQLQKSRTOLEVLVAGASILLALL 74  
QY 121 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 180  
Db 75 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 134  
QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORFYLSCLQVERIEELGAOP 240  
Db 135 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORFYLSCLQVERIEELGAOP 194  
QY 241 LRDLIEKIGGMNITGPMDDNFMFVILKAVAGTRATPFTVYISADSKSNSNVIOVDOS 300  
Db 195 LRDLIEKIGGMNITGPMDDNFMFVILKAVAGTRATPFTVYISADSKSNSNVIOVDOS 254  
QY 301 GLFLPSRDYILNRTANEKVLTAVIDYMEELGMLGGRPTSTREMOQVLELEIQLANITY 360  
Db 255 GLFLPSRDYILNRTANEKVLTAVIDYMEELGMLGGRPTSTREMOQVLELEIQLANITY 314  
QY 361 PDGRDEEKIYHKMSISELOALAPSDMWLEFLSLSPLEISDSSEPVVYVGMVDYLOQVS 420  
Db 315 PDGRDEEKIYHKMSISELOALAPSDMWLEFLSLSPLEISDSSEPVVYVGMVDYLOQVS 374  
QY 421 ELINRTEPSILNNYLIMNLVOKTSSLDRRFESAOKLETLTYGTKKSCVPRMOTCISNT 480  
Db 375 ELINRTEPSILNNYLIMNLVOKTSSLDRRFESAOKLETLTYGTKKSCVPRMOTCISNT 434  
QY 481 DDALGFALGSLFYKATFDROSKEIABGMISEIRTAFEALGOLVWMDKTRQAKAKADA 540  
Db 435 DDALGFALGSLFYKATFDROSKEIABGMISEIRTAFEALGOLVWMDKTRQAKAKADA 494  
QY 541 IYMGIPDFILPEKELDVIDYGEISEDSFQOMNLNLYNFSKAVADOLRKPSRDOS 600  
Db 495 IYMGIPDFILPEKELDVIDYGEISEDSFQOMNLNLYNFSKAVADOLRKPSRDOS 554  
QY 601 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARNHPKALNFGGIGVWNGHELTHAFDQGRE 660  
Db 555 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARNHPKALNFGGIGVWNGHELTHAFDQGRE 614  
QY 661 YDKEGMLRPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGJLKAAY 720  
Db 615 YDKEGMLRPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGJLKAAY 674  
QY 721 NAKAWLARKHGEEQQLPAVGLTNHQLFPVGFQAVWCVRTPSSHGLVTDPHSPARFRV 780  
Db 675 NAKAWLARKHGEEQQLPAVGLTNHQLFPVGFQAVWCVRTPSSHGLVTDPHSPARFRV 734  
QY 781 LGTILNSRDLRHFQCGVSPMNPQOLCEW 811  
Db 735 LGTILNSRDLRHFQCGVSPMNPQOLCEW 765

RESULT 5  
US-09-667-373-4  
; Sequence 4, Application US/09667373  
; Patent No. 6524840  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6524840el Human Endothelin Converting  
; TITLE OF INVENTION: Enzyme-Like Proteins and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0043-USA  
; CURRENT APPLICATION NUMBER: US/09/667,373  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/156,102  
; PRIOR FILING DATE: 1999-09-24

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: PRIOR APPLICATION NUMBER: US 60/176,689
: PRIOR FILING DATE: 2000-01-18
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 893
: TYPE: PRT
: ORGANISM: homo sapiens
US-09-667-373-4

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Query Match	89.2%	Score 3820	DB 4	Length 883
Best Local Similarity	97.8%	Pred. No. 0		
Matches 726	Conservative	5	Mismatches 9	Indels 2
				Gaps 1

Oy	70	WRVYCPHRSIISGLCARWYVFOKRGROLISGRTLEVLWAGASITLALALGLVALGV	139
	144	WYSSSECVHTVDVLSB--VGFQKRGROLISGRTLEVLWAGASITLALALGLVALGV	201
Db	130	QYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFYQFSCGMIRNPPLPDRSSMWT	189
Oy	202	QYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFYQFSCGMIRNPPLPDRSSMWT	261
Db	190	FNSLMDONQALIKHLENTTENSSEAEOKTORFLISCLQYERIBELGAOPLRLIRKIG	249
Oy	262	FNSLMDONQALIKHLENTTENSSEAEOKTORFLISCLQYERIBELGAOPLRLIRKIG	321
Db	250	GMNITGMPDDNFMEVLKAVAGYRATPFYIYISADSSNSNVIQVDSGLFLPSRDY	309
Oy	322	GMNITGMPDDNFMEVLKAVAGYRATPFYIYISADSSNSNVIQVDSGLFLPSRDY	381
Db	310	YLNRATANEXYLTAIYLDYMEELGMLLGGRTSTREMOQVLELEIQLANITVPQDRDEE	365
Oy	382	YLNRATANEXYLTAIYLDYMEELGMLLGGRTSTREMOQVLELEIQLANITVPQDRDEE	441
Db	370	KIYHKNSISELOALPSMDLEFLSTLSPLBSDBEPVYVYGMVYDLOQVSELINRTEPS	422
Oy	442	KIYHKNSISELOALPSMDLEFLSTLSPLBSDBEPVYVYGMVYDLOQVSELINRTEPS	501
Db	430	ILNNYLIWNIWOKTTSSLDLRPESAEKLELTLYGKKSCVPRWOTCISNTDDALGFPLG	489
Oy	502	ILNNYLIWNIWOKTTSSLDLRPESAEKLELTLYGKKSCVPRWOTCISNTDDALGFPLG	561
Db	490	SLFPAKAFDRQSKRIBEGMISEIRTAFFEBALGOLVWMEKTRQAKERADAIDYMGPPD	549
Oy	562	SLFPAKAFDRQSKRIBEGMISEIRTAFFEBALGOLVWMEKTRQAKERADAIDYMGPPD	621
Db	550	FILEPKELDVIYDGYEISEDSFQONMLNINYSAKYMAODLRKPPSRQMSNTQYUNAY	609
Oy	622	FILEPKELDVIYDGYEISEDSFQONMLNINYSAKYMAODLRKPPSRQMSNTQYUNAY	681
Db	610	YLPFKNBIIVPAPGILQAPFARNRHPKALNFGGIVGVMGHELTHAADDGREYDEKGNLPR	665
Oy	682	YLPFKNBIIVPAPGILQAPFARNRHPKALNFGGIVGVMGHELTHAADDGREYDEKGNLPR	741
Db	670	WMQNESLAAFRNHTACMEQYNOYQVNGERLINGRQTLGENTIDNGGLXAAVNAAYKMLRK	729
Oy	742	WMQNESLAAFRNHTACMEQYNOYQVNGERLINGRQTLGENTIDNGGLXAAVNAAYKMLRK	801
Db	730	HGEEOQLPAVGLTNHQLFYVGAQWCVSRTPBSSHGELVTDPHSPAFPRVLGTLNSRD	789
Oy	802	HGEEOQLPAVGLTNHQLFYVGAQWCVSRTPBSSHGELVTDPHSPAFPRVLGTLNSRD	861
Db	790	FLHRHGGCPVGSPPMNPQGLCEWV	811
Oy	862	FLHRHGGCPVGSPPMNPQGLCEWV	883

RESULT 6  
US-08-574-763-2  
; Sequence 2, Application US/08574763  
; Patent No. 5753576  
; GENERAL INFORMATION:  
; APPLICANT: Yanagisawa, Masashi

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Query Match	85.5%	Score 3662;	DB 1;	Length 787;
Best Local Similarity	93.0%	Pred. NC. 0;		
Matches 690;	Conservative 22;	Mismatches 28;	Indels 2;	Gaps 1;

Qy	70	WRTCHSIAHSISGLSRMTWQOKTROLLSRFOLEYUAGASILAAALLIGVLAV	129
	48	WTVSSGVCHTVDOVLNE - AGRKRTSKSLGLHFOLEVLAVGSLILAAALLIGVLAV	105
Qy	130	QYHRDESHSTCTTEACIRVAKGILIESLDRGVSPCEDFYQSPCGWIRNPLPDRSHMNT	189
Db	106	QYHRDPSHSTCTTEACIRVAKGILIESLDRGVSPCEDFYQSPCGWIRNPLPDRSHMNT	165
Qy	190	FNSLMONOAILKHLENTFNTSSSEABOKTORFPLSTCLOYERIEELGAOPLDILKIG	249
Db	166	SNLSMOONQAILKHLENTFNTSSSEABOKTORFPLSTCLOYERIEELGAALNDLIDKIG	225
Qy	250	GNMTITPMDQDNFMEYLKAVACTYATPFTVYIISADSKSSNVIQVDSGLFLPSRDY	309
Db	226	GNMTITPMDQDNFMEYLKAVACTYATPFTVYIISADSKSSNVIQVDSGLFLPSRDY	285
Qy	310	YLNRTANEKYLTAVIDYMEELGMLLGGPPTSRREMOQVLELEQLANITVPDQDRDEE	369
Db	286	YLNRTANEKYLTAVIDYMEELGMLLGGPPTSRREMOQVLELEQLANITVPDQDRDEE	345
Qy	370	KIYHKNSISELOALAPSMDWLEFLSPILSPLESDSEBVVYGYMDYLQOVSSELINTREPS	429
Db	346	KIYHKNSIAELOALAPSMDWLEFLSPILSPLESDSEBVVYGYMDYLQOVSSELINTREPS	405
Qy	430	ILNNYLIIMLVNQKTTSSLDPRPESAOEKLLETIVGTKKSCVPRQOTCISNTDIALPAGL	489
Db	406	ILNNYLIIMLVNQKTTSSLDPRPESAOEKLLETIVGTKKSCVPRQOTCISNTDIALPAGL	465
Qy	490	SLFVKATPDRQSKETIAEGMISIRAFPEALGOIWMDEKTRQAKAKADAYDMIGFPD	549
Db	466	SLFVKATPDRQSKETIAEGMISIRAFPEALGOIWMDEKTRQAKAKADAYDMIGFPD	525
Qy	550	FLIEPEKLDVDYDGYHISDFSPQNMVLNYPASAAWADQLRKPPSDQMSMTPTQYNAV	609
Db	526	FLIEPEKLDVDYDGYHISDFSPQNMVLNYPASAAWADQLRKPPSDQMSMTPTQYNAV	585

QY 610 YLEPTKEIVPAGILQAPFYARNHPKALNFGIGVNGHELTHAFDDQREYDKENLRP 669  
DB 586 YLEPTKEIVPAGILQAPFYARNHPKALNFGIGVNGHELTHAFDDQREYDKENLRP 645  
QY 670 WQNESIAAFRNHTACMEBOYNQVNGERLNGRQTLGENTADNGGLKAAYNAYKAMLRK 729  
DB 646 WQNESIAAFRNHTACMEBOYSOVYNGEKLNGRQTLGENTADNGGLKAAYNAYKAMLRK 705  
QY 730 HGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPPSPARFVLGTLNSRD 789  
DB 706 HGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPPSPARFVLGTLNSRD 765  
QY 790 FLRHFGCPVGSPPMNPQGLCEW 811  
DB 766 FLRHFGCPVGSPPMNPQGLCEW 787

RESULT 7  
US-08-646-273-36  
; Sequence 36, Application US/08646273  
; Patent No. 6066502  
; GENERAL INFORMATION:  
; APPLICANT: Kroeger, Burkhard, Seuburger, Harald, Meyer, Thomas, Schmidt,  
; APPLICANT: Martin, Jacob, Blard, Oter, Rainer, Subkowski, Thomas, Hilten, Heinz.  
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Keil & Weinkauff  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: Wordperfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,273  
; FILING DATE: 16-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/03706  
; FILING DATE: 11-NOV-1994  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 753 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-646-273-36

Query Match 60.5%; Score 2590.5; DB 3; Length 753;  
Best Local Similarity 60.1%; Pred. No. 6.8e-242;  
Matches 481; Conservative 122; Mismatches 148; Indels 49; Gaps 6;

QY 14 MVEYKATLDEDAPEPTVEGASPDAMEVGKASPPSPGSPGMPGTRSSGLFWRT 73  
DB 1 MSTEYKATLDEBLDVLSREGDAVPNGLQVNF-----HSRSGQRGW--- 42  
QY 74 CPHLRSSGLCSRTMVGFOGKTRQLGSRPQLBELVLAGASLLAALLGLGLVLAGVYH- 132  
DB 43 -----AAKQVERKRLVTLVLAAGLVAACLALGIGYOT 76  
QY 133 RDPSSHSTCLTEACIRVAGKILIESLDKRGVSPCEPFYQFSCGWIIRNPLPDGRSRMTFNS 192  
DB 77 RSP--SVCSSEACVSIVSSILSSMDPTVDDCHDFPSVACGWMKANVPDGRHMGFSN 134  
QY 193 LMTDNQAILKLLLENTFNSSSEAEQKTFYLSCLQVERIEBELGAQPLDLIEKIGWN 252  
DB 135 LMEHNOAILIKLLENST-ASVSEAEKRAQYYRAQNMETRIEELRAKPLMELIERLIGWN 193

QY 253 ITGPMQDNFMEVLAQVACTYATPPTFYISADSKSSNSNVIQVDSGLFLPSRDYLN 312  
DB 194 ITGPMQDNFMEVLAQVACTYATPPTFYISADSKSSNSNVIQVDSGLFLPSRDYLN 253  
QY 313 RTANERYLTAYLDYMELEML-GRPTSTREMOQVLELEIOLANITTYPODORREBEK 371  
DB 254 KTENEYVLQGLYNNYQQLKLGGEDEAIRPMQOILDEFLANITTYPODORREBEK 313  
QY 372 YHKMSISEIOLAPSMWLEFLSLPSLESDSEVVVYGMQVLAQVSELINRTPSIL 431  
DB 314 YHNTYAEIQTALPAINMLPFLNTIYVVEINSEPIVYDKYLEFOISTILINTTRCL 373  
QY 432 NNTLWNLVQKTTSLDRRRESAOKELTLYGTKSCVPRMOTCSINTDALGALGSL 491  
DB 374 NNTLWNLVQKTTSLDRRRESAOKELTLYGTKSCVPRMOTCSINTDALGALGSL 491  
QY 492 FYKATFDROSKETAEEMISEIRTAPEBALGOLVWDEKTRQAAKEADAIYDMIGPDDI 551  
DB 434 FYKATFDROSKETAEEMISEIRTAPEBALGOLVWDEKTRQAAKEADAIYDMIGPDDI 551  
QY 552 LEPKELDVYDGEISEDSFPQNMNLVNFSAKVMDOLRKPSRPMQMTPTQVAYYL 611  
DB 494 MDEKELDVYDGEISEDSFPQNMNLVNFSAKVMDOLRKPSRPMQMTPTQVAYYL 611  
QY 612 PTKEIVPAGILQAPFYARNHPKALNFGIGVNGHELTHAFDDQREYDKENLRP 671  
DB 554 PTKEIVPAGILQAPFYARNHPKALNFGIGVNGHELTHAFDDQREYDKENLRP 671  
QY 672 QNESIAAFRNHTACMEBOYNQVNGERLNGRQTLGENTADNGGLKAAYNAYKAMLRK 731  
DB 614 QNESIAAFRNHTACMEBOYSOVYNGEKLNGRQTLGENTADNGGLKAAYNAYKAMLRK 731  
QY 732 EEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPPSPARFVLGTLNSRD 791  
DB 674 EEOQLPAVGLTNHOLFVGFPAQVWCVRTPRESSHEGLVTDPPSPARFVLGTLNSRD 791  
QY 792 FLRHFGCPVGSPPMNPQGLCEW 811  
DB 734 FLRHFGCPVGSPPMNPQGLCEW 787

RESULT 8  
US-08-646-273-30  
; Sequence 30, Application US/08646273  
; Patent No. 6066502  
; GENERAL INFORMATION:  
; APPLICANT: Kroeger, Burkhard, Seuburger, Harald, Meyer, Thomas, Schmidt,  
; APPLICANT: Martin, Jacob, Blard, Oter, Rainer, Subkowski, Thomas, Hilten, Heinz.  
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Keil & Weinkauff  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: Wordperfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,273  
; FILING DATE: 16-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/03706  
; FILING DATE: 11-NOV-1994  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 754 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-273-30

Query Match 60.0%; Score 2567.5; DB 3; Length 754;  
Best Local Similarity 59.6%; Pred. No. 1.2e-239;  
Matches 477; Conservative 119; Mismatches 154; Indels 51; Gaps 7;

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14 MVEKATLDEDEPPEVPGASPDMEVG-KGASPFSGSPGCMPTGPRSSGLFMRV 72
2 MSTYKRLPEDELDVDSLSDDVYFNHLQVNFGR-----PRNGQRCW-- 43
73 TCEHRSISGLCSRTWGFQKGTROLGSRTOLEVLGASILLALLGLVALGVQYH 132
44 -----AARTPVKRLVALLAALVACLAVLGIGYQ 76
133 -RDSHSTCTEACIRVAGKILSLDRGVSPCEDFYQSCGGWIRNPLPDGSRMNTFN 191
77 TRTP--SVCLSEACISVTSILSSMDPTVPCQDFPYACGGMKAPVPDGHSGRMGTF 134
192 SIMDONALIKHLENTFNSSSAEQKQRYLSCQVERIEELAQPLRDLIEKIGW 251
135 NLMEHNOAIIKHLENT--ASVSEAKRDEYRACNETRIBELKAKPLMELIEKLGW 193
252 NITGPMODNFMELKAVAGTYRATPEFYVYISADSKSNSNVIOVDSGLFLPSRDY 311
194 NITGPMKDNFQDLOVTSHTSHYSPFVSADSKSNSNVIOVDSGLFLPSRDY 253
312 NRTANEKVLTAVIDYMEELGMLGGRPTST-REQMOVLELEIQLANITVPQDRDEK 370
254 NKTENEKVLGYLVNMQGLKLGAGADITRPMQOILDFETALANITTPQEKGRDEEL 313
371 IYHKMSISELOALAPSDMLEFLSLPLELSDSEPVVYVYGMVLOQVSELINRTPSI 430
314 IYHKVTAELQTLAPALNMLPELNTIYPAVINESEPIVYDKELYSKVTSLNIDKCL 373
431 LNNYLNMLVQKTTSLDRPESAEKLETLTGKKSQVPRMOTCISNTDAGFALGS 490
374 LNNYMINLVKRTSSFLDQRFQDADEKFMVMTGKTCCLPRMFCVSDTEMLTGFLGP 433
491 LFKVATPDROSKEIAEGMISIRTAPEBALGQLVMDKTRQAAEKADAIYDMIGPDP 550
434 MFVATPAEDSKNIASEIILEIKKAFESLSTLKMDEBTRKSAKERADAIYNNIGYPNF 493
551 ILKEKLDVYDGEISBDSFQOMMLYNFSAVMDQARPKSPROMSTPOTVNAVY 610
494 IMDEKLDKVPNDTAVPDLYFENAMRPFNFMSRVLTADQLKAKNRQMSSTPVMNAVY 553
611 LPTGNEIVFPAGILQAPFYARNHPRKALNFGSIGVVMGHELTAFDDQGREYDEKGNLRPW 670
554 SPTGNEIVFPAGILQAPFYTRSSPNALNFGSIGVVMGHELTAFDDQGREYDEKGNLRPW 613
671 WONESLAFRNHTACMEBOYNQYOVNGERLNGROTIGENIADNGLKAAVNAVYAWLRKH 730
614 WKNSSVBAFQKQOTACMEQYGVNGEVPVGRHTLENIADNGLKAAVNAVYQWNVKYN 673
731 GEEQOLPAVGLTNHQLPFGVPAQVWCVTRPESHEGLVMDPHSPARFVLTGITSNRDF 790
674 GAEOYLLPFLGLTNQLPFLSPAQVWCVTRPESHEGLITDPHSPSRFVLTGITSNRDF 733
791 LRHFQCPGVSPMNPQGLCEW 811
734 SEHFHCPPGSPMNPHHKCEW 754
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## RESULT 9

US-08-289-112-2  
Sequence 2, Application US/08289112  
Patent No. 568640

GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi  
TITLE OF INVENTION: Endothelin Converting Enzyme-1: A  
TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The

TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA

ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/289,112  
FILING DATE: 10-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:414/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEO ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-289-112-2

Query Match 59.5%; Score 2546; DB 1; Length 758;  
Best Local Similarity 59.8%; Pred. No. 1.4e-237;  
Matches 474; Conservative 118; Mismatches 160; Indels 40; Gaps 7;

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23 RDEDAETP-VBEGASPDMEVGKASPPSPGCMPTGTPRSSGLFMRVTCPHLSIS 81
4 RGODLRSPLLSSEAP-----GLTSSPRLPSPLOVNRGRNRCW----- 47
82 GLCSRTWGFQKGTROLGSRTOLEVLGASILLALLGLCLVALGVQYH-RDPSHSTC 140
48 -----AARTPVEKRLVALLAALVACLAVLGIGYQRTT--SVC 87
141 LTRACIRVAGKILSLDRGVSPCEDFYQSCGGWIRNPLPDGSRMNTFNLSMDONQAI 200
88 LSEGCTSVTSILSSMDPTVPCQDFPYACGGMKAPVPDGHSGRMGTFSNLMENHOAI 147
201 LKHLLENTFNSSSEAEKQRYLSCQVERIEELAQPLRDLIEKIGMNTGPMPOD 260
148 IKHLENT--ASVSEAKRQVYRACMETRIBELKAKPLMELIEKLGAMNITGPMPOD 206
261 NMEVILKAVAGTYRATPEFYVYISADSKSNSNVIOVDSGLFLPSRDYILKRTANEKYL 320
207 NFDPTLQVVTSHHTSPFVSADSKSNSNVIOVDSGLFLPSRDYILKRTANEKYL 266
321 TAYLDYMEELGMLGGRPTST-REQMOVLELEIQLANITVPQDRDEKITYHKMSISE 379
267 TGYLNTVVOGLKLGAGADITRPMQOILDFETALANITTPQEKRRDELYHKVTAAB 326
380 LGALAPSDMLEFLSLFLSLPDESPVYVYGMVLOQVSELINRTPESILNNTYINML 439
327 LGTLAPALNMLPELNTIYPAVINESEPIVYDKELYSKVTSLNIDKCLANNYMINML 386
440 VQKTTSLDRPESAEKLETLTGKKSQVPRMOTCISNTDAGFALGSLEFVKATPDR 439
387 VRKTSFLDQRFQDADEKFMVMTGKTCCLPRMFCVSDTEMLTGFLGPMVKATFAE 446
500 QSKYELIAGMISIRTAPEBALGQLVMDKTRQAAEKADAIYDMIGPDPFLIEPELDD 559
447 DSKNIASEIILEIKKAFESLSTLKMDEBTRKSAKERADAIYNNIGYPNIFMDPELDK 506
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QY      560 VYDGEISDSSEFQNNLNIYNFSKAYMAOULRKPFRDOMSMTPOCVNAYLTPTXKEIYF   619
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      507 VFNDTAVADYLXFENAMREFNFSSKRVTALDQLRKAFPRDOMSKMTPPMVNAVYSTTKNEIYF   566

QY      620 PAGILQAPFYAKNHHPKALNFGGIGVVMGHETLHAFDDGREYDKGNLRPMWONESLAAP   679
       ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      567 PAGIIQAPPYTRSSPVALNFFGGIVGVVGHETLTHAFPDDGREYDKDNLRPMWNKSIVEAF   626

QY      680 RHHTCMEEQYNOYQVNGERLNGROTLGENIADNGGLKAANYAKMLRKHEEQOLPAV   739
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      627 KQOTCAWEQYNYNSNGEPPVNGRHITLGINIDNGGLKAYRAYQYMWKNKGAEQTLPVL   686

QY      740 GLTNHQLFVGFQAQVWCSVRTPESSHGAVTDPHSAPRFVLGTLLSNSRDLFLRHPCGPYV   799
       ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      687 GLTNQOLFPLSGQVWC SVRTPESSHGELITDPHSFRFRVIGSINSKFESHFHCPRG   746

QY      800 SPMPNQCLCEW   811
       ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      747 SPMPNHKCEW   758

RESULT 10
US-08-646-273-23
; Sequence 23, Application US/08646273
; Patent No. 6066502
GENERAL INFORMATION:
APPLICANT: Kroeger, Burkhard, Seubberger, Harald, Meyer, Thomas, Schmidt,
APPLICANT: Martin, Jacob, Elard, Oeter, Rainer, Sudkowski, Thomas, Hille, Heinz
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauff
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
OPERATING SYSTEM: IBM AT-compatible, 80486 processor
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,273
FILING DATE: 16-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03706
FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-273-23

Query Match          59.3%; Score 2539.5; DB 3; length 708;
Best Local Similarity 64.8%; Pred. No. 5,4e-237;
Matches 461; Conservative 110; Mismatches 135; Indels 5; Gaps 4;

QY      103 TQLELVLAGASILLAAALLLGCVAGVOYH-RDPSHSTCTREACTRVAGKIIESLDRGS   161
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1 TPVEGRLLVVVALLAALVAACLANVLGIQYQTRP--SVLSERACISVTSIILSMDDPV   58

QY      162 PCEDFYQSCGCGWIRRNPIPDGRSRWNTFNLSIMDONQAILKHILLENTFNSSSEABQKTQ   221
       ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 PCODEFTYAACGMKANIPVDGHSRWGTFSNMENHOAIKKHLLENST-AVSSEARXQQ   117

QY      222 RFYSLCQVERIEELGAQPLRIETKIGWMNTGPMDOONFEVYLKAVAGTYRAFPFTV   281
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118 EYRAQCNMETRIEELKAKRLMELIEDGGMNITGPMDKONFDOTLQAVVSHYHTSPFSV   177

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QY 282 ITSDSKSNSNVIOVDOSGFLPSRDYYLNRTAKEKYLTAVALDYMEELGMLGGRPST 341
Db 178 YVSADSKSNSNVIOVDOSGIGLPSRDYYLNRTEKEKYLITGLANTVQGLKGGGAET 237
QY 342 -REQMOVLELEIOLANITVPDORDEDEKIYHKNSISELQALASMDWLEFLSPLSL 400
Db 228 IRPQMOQLDDEPITALANITITPEKKRDEELIYHKVTALEQLQTLAPAINMLPFLNTIFYV 297
QY 401 ELSDEPVPVYGM DYLOQVSEILNRTEPSILANNYLINMLVOKTTSLSLDRPESAOEKL 460
Db 298 EINESEPIVIDKEYLSKYSTLINSTDKCLANNWIMLVKRTSSFLDQFQDADEKEME 357
QY 461 TLVYKKSQVRRMOCISINTDDALGFALGSLFKVATPDRROSKEIABGMSLRTAFEBAL 520
Db 358 VMGTGKTKCLPRMKCVSDETERNTLGFALGPMFVKATPABDSKNISSEIILEKKAPEEL 417
QY 521 GQLVWMDERTQAAEKADAIYDMIGPPDFILEPEKLDVYDGYEISEDSFPQNMILYN 580
Db 418 STLKMMDEBTRKSAEKADAIYNNMIGYDNFIMDPKELDKVFNDYAVPDLVEYENMRFPN 477
QY 561 FSAKYMADQLKPPSRDQSMSTPQTVNAYTLPTKKEIYFPAGILOAPFTARHPKALNG 640
Db 478 FSWRVTADQLKAPRDQSMSTPPMVNAYYSPTKNEIYFPAGILOAPFTARSSPVALNG 537
QY 641 GIGVWGHETLHAFPDQGREYDEKGNLRPMWONESLAPFRNHTACMBEYQNOYNGERL 700
Db 538 GIGVWGHETLHAFPDQGREYDKGNLRPMKNSSVEAFKQOTACMDEYQNGYSNGEYV 597
QY 701 NGROTIGENIADNGELKAAVYAKMLRKHGEQQLPAVGLTNNQLFPVGAQVACSVET 760
Db 598 NGRHTIGENIADNGELKAAVYQVWVKKNGAEQTLPTLGLTNNQLFLSFAQVACSVET 657
QY 761 PESSHEGLTDPHSPARPRVYGLTSSNRDPLRHPCCPGSPNNQOLCEW 811
Db 658 PESSHEGLTDPHSPSRFRVIGISSNKFSEHFHCPGSPNNPHKCEW 708

RESULT 11
US-08-646-273-25
/ Sequence 25, Application US/08646273
/ Patent No. 6066502
/ GENERAL INFORMATION:
/ APPLICANT: Kroeger, Burkhard, Seuilberger, Harald, Meyer, Thomas, Schmidt,
/ APPLICANT: Martin, Jacob, Elard, Otfert, Rainer, Subkowski, Thomas, Hillen, Helinz
/ TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Keil & Weinkauff
/ STREET: 1101 Connecticut Avenue
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM AT-compatible, 80486 processor
/ OPERATING SYSTEM: MS-DOS version 6.0
/ SOFTWARE: Wordperfect version 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646, 273
/ FILING DATE: 16-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP94/03706
/ FILING DATE: 11-NOV-1994
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein

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US-08-646-273-25

Query Match 59.2%; Score 2534.5; DB 3; Length 703;

Best Local Similarity 65.4%; Pred. No. 1,66-236; Matches 458; Conservative 113; Mismatches 124; Indels 5; Gaps 4;

114 LILAAALIGLVALGVYH-RDPSHSCTCTEACIRVAGKILIESIDRGVSPCEDFYQSCG 172  
 7 VLLAAGVACIALALGIQYGRSP--SVCSBACVSVSSILSSMDPVDCHFFSVACG 64  
 173 GWIRNPLPDGRSMNTFNSLMDONAILKHLLENTFNSSSEAEQCTRFYLSCLQVER 232  
 65 GWIKANVPDGHSGWGTFSMLWBNQAIILKHLLENST-ASVSEAEKQYVYRAQNMETR 123  
 233 IIEELGAPRLDLKELIGMNITGPMDDNMEVYLKAVAGYRATPPTVYISADSKSNS 232  
 124 IIEELRAPRLLELRLGGMNITGPMADNFODTLQVYTAHRTSPFVSYSADSKSNS 183  
 293 NVIQVDSGLFLPSRDYILNRTANEKVLTAVALDYMEELGMLL-GGREPTREOMQVLEL 351  
 184 NVIQVDSGLFLPSRDYILNRTANEKVLTAVALDYMEELGMLL-GGREPTREOMQVLEL 243  
 352 EIOLANITVPDQDRDEKLYHKMSISELQALAPSMWLEFLSLPSLELSDSEPVVY 411  
 244 ETALANITTIPOEKRRDEELIYHKVTAELQTLAPALNMLPLNTIIFYVEINSEPIVY 303  
 412 GMYLOOVSELINRTESILNNTYILNMLNOKTSSLDREPSAEKLETLTGTKSCVP 471  
 304 DKLEYLSTILINTDRCLNNTYIMLVKRTSSFLDQRFODADEKMEVYGTGKTCCLP 363  
 472 RMQTCISNTDAGLFGALGSLFVKATPDRQSKIEAGMISEIRTAFEALGOLVMDDEKTR 531  
 364 RMKFCVSDTENNLGALGPMFVKATFADSKSTATETILIKKAFESLSTLKMDDETR 423  
 532 QAAKEKADAIYDMIGPFDLLEPKELDDVYDGEISEDSFPQMLNLVNSAKYADQLR 591  
 424 KSAKEKADAIYNNIGYENFTMDPKELDKVNDYAVDLVFEENAMREFNSWRTADQLR 483  
 592 KPSRDQSMTPQVNAVYVLPTKNEIYFPAGILLOAPYARNHPKALNFGIGVVMGHELT 651  
 484 KAPRDMQSMTPQVNAVYVPTKNEIYFPAGILLOAPYARNHPKALNFGIGVVMGHELT 543  
 652 HAFDQGREYDEKGNLRFPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIA 711  
 544 HAFDQGREYDEKGNLRFPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIA 603  
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 604 DNGGLKAAVAYKAKMLRKGBEQQLPAVGLTNHQLFTVGAQVWCYVTRPSSHEGLVTD 663  
 772 PHSAPRVRVIGTSLNSRDLRHCPCPGVSPMNPQQLCEW 811  
 664 PHSAPRVRVIGTSLNSRDLRHCPCPGVSPMNPQQLCEW 703

RESULT 12

US-08-646-273-19

Sequence 19, Application US/08646273

Patent No. 6066502

GENERAL INFORMATION:

APPLICANT: Kroeger, Burkhard, Seubberger, Harald, Meyer, Thomas, Schmidt,

APPLICANT: Martin, Jacob, Blard, Ofter, Rainer, Subkowski, Thomas, Hilten,

TITLE OF INVENTION: Bodochelein Converting Enzyme (BCE).

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Keil &amp; Weinlauf

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM AT-compatible, 80486 processor  
 OPERATING SYSTEM: MS-DOS version 6.0  
 SOFTWARE: WordPerfect version 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,273  
 FILING DATE: 16-NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP94/03706  
 FILING DATE: 11-NOV-1994  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 567 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-273-19

Query Match 47.8%; Score 2047; DB 3; Length 567;

Best Local Similarity 65.5%; Pred. No. 2,36-189; Matches 372; Conservative 92; Mismatches 102; Indels 2; Gaps 2;

183 GRSRNTFNSLMDONAILKHLLENTFNSSSEAEQCTRFYLSCLQVERIEELGAPLR 242  
 1 GHSRMTGFNSLWBNQAIILKHLLENST-ASVSEAEKQYVYRAQNMETRIELKAKPLM 59  
 243 DLIEKIGGNITGPMDDNMEVYLKAVAGYRATPPTVYISADSKSNSNYIQVDSGL 302  
 60 ELIEKIGGNITGPMDDNMEVYLKAVAGYRATPPTVYISADSKSNSNYIQVDSGL 119  
 303 FLPSRDYILNRTANEKVLTAVALDYMEELGMLLGGREPTST-RBOMQVLELQIANITVP 361  
 120 GYPSRYILNRTANEKVLTAVALDYMEELGMLLGGREPTST-RBOMQVLELQIANITVP 179  
 362 QDORDEKLYHKMSISELQALAPSMWLEFLSLPSLELSDSEPVVYGYDYLQVSE 421  
 180 QEKRRDEELIYHKVTAELQTLAPALNMLPLNTIIFYVEINSEPIVYDKEYLSKVT 239  
 422 LIRTEPSILNNTYILNMLNOKTSSLDREPSAEKLETLTGTKSCVPKMTQTCISND 481  
 240 LIRTEPSILNNTYILNMLNOKTSSLDREPSAEKLETLTGTKSCVPKMTQTCISND 299  
 482 DALGFGALGSLFVKATPDRQSKIEAGMISEIRTAFEALGOLVMDDEKTRQAAKEKADAI 541  
 300 NTLGFGALGPMFVKATFADSKSTATETILIKKAFESLSTLKMDDETRKSAKEKADAI 359  
 542 YDMIGPFDLLEPKELDDVYDGEISEDSFPQMLNLVNSAKYADQLRKPSRDQSM 601  
 360 YNNIGYENFTMDPKELDKVNDYAVDLVFEENAMREFNSWRTADQLRKAPNRDQSM 419  
 602 TPQTVNAVYVLPTKNEIYFPAGILLOAPYARNHPKALNFGIGVVMGHELTAFDDQGREY 661  
 420 TPQTVNAVYVPTKNEIYFPAGILLOAPYARNHPKALNFGIGVVMGHELTAFDDQGREY 479  
 662 DKEGNLRFPMWQNESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAAVY 721  
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 722 AYKAMLRKGBEQQLPAVGLTNHQLFTV 749  
 540 AYONVWKKGAEQTLPTLGLTNNOFLFL 567

RESULT 13

US-09-704-611-2

Sequence 2, Application US/09704611

Patent No. 6548284

GENERAL INFORMATION:

APPLICANT: JCR Pharmaceuticals Co., Ltd.

TITLE OF INVENTION: Membrane-bound Metalloprotease and Soluble Secreted Form There

FILE REFERENCE: GP30

CURRENT APPLICATION NUMBER: US/09/704,611

CURRENT FILING DATE: 2000-11-03



Search completed: July 3, 2004, 20:09:28  
Job time : 24 secs

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/ GENERAL INFORMATION:
/ Applicant: SmithKline Beecham Plc
/ Title of Invention: No. 6255468el Compounds
/ File Reference: GP30124
/ Current Application Number: US/09/305,640B
/ Current Filing Date: 1999-05-05
/ Number of Seq ID Nos: 4
/ Software: FastSeq for Windows Version 3.0
/ Seq ID No 2
/ Length: 775
/ Type: PRT
/ Organism: Homo sapiens
/ US-09-305-640-2

Query Match      32.6%; Score 1397; DB 3; Length 775;
Best Local Similarity 36.6%; Pred. No. 4.9e-126;
Matches 295; Conservative 150; Mismatches 272; Indels 90; Gaps 19;

Qy      34 GGASPDAMEYKASPPSPGSPGTPGTPSSGLFW--RVTCPHLRSISGLCSRTWVGF 91
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Db      67 -----VFNAGLCAILAAMLAALKYLGPVAAAG-----GAC-PRGCPPE 101
Qy      146 ----IRVAGKILSLDRGVSPCEDEYQFSGGWIIRRNPLPDGRSRMWTFSIMDONAIL 201
Db      102 RKAFAARAFLANLDSIDPCDFYFACGWMRRHALPDDKLTGTIAIGQNEERL 161
Qy      202 KHLLENTFSSSEAEQKQRFYLSCLQVERIEELAQPLRDLIEKIGWNITGP----- 256
Db      162 RRLIARPGGPGGAQKNAAFRSCLDMEIERLGRPLMEVIEDCGMDLGAEERPG 221
Qy      257 ----WDQDNMEVLKAVAGTYRATPFTTYISADSKSSNSNVIQVDQGLFLPSRDYLN 312
Db      222 VAARMDLN--RLLYKAQGYSAALFSLTVSLDRNSSRYVIRIDQGLTLPERLYLA 278
Qy      313 RTA--NEKVLTAAYLDYMEELGMLGGRTSTRBQOQVLELEIOLANTVPO--DORRDEE 369
Db      279 QDEDSKILAAVYFMERVLSLGA--DAVBQKAQELIQQEQLANTVSEYDRLRDVS 336
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Db      337 SMYNKVTLGQLQKITPHLRW---KWLDDQIPEDESEEBEVVLATDYMQVSQLIRST 392
Qy      427 EBSILANNYLIMLVQKTTSSLDRFESAQEKLETLVGTKSCVPR--WQTCISNTDDAL 484
Db      393 PHRVLNHYLVWRVVVVLSEHLSPFREALHELAQEMEGSDK--PQELARVCLGQANRHF 449
Qy      485 GFALGSLFVKATPDRSGKEIABGMISIRTAFAFEALGOLVWMDKTRQAAKERADATYDM 544
Db      450 GMLGALFVEHNSASKAKAVQQLVEDIKITLIGQRELEDMWDAETRAAARAKIQYMMVM 509
Qy      545 IGPPDFILBEKELDDVYDYEISEDSPFQMLNLVNPASAKVMDQLRKPSPDQWSMTPQ 604
Db      510 VGYPDFLTKDADVADKEYE--FEVHEKTYFKNIILNIRFSIQLSVKIKIQEVDKSTWLLPQ 568
Qy      605 TVNAYYIPTQNEIYFPGIILQAPFYARNHPKALNFGSIGVMGHELTTHAFDDQREYDK 664
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Qy      665 GNLRPWQNESLAFRNHTACMEQYQYOVNGERLNGROTIGENIADNGGLKAAYAYK 724
Db      629 GNLHMTWTEASYSFLKAEIYALYNDFTVYNQVNGKHLGENIADMGGKLAIYAYQ 688
Qy      725 AMLRKGEEOQLPAVGLTNHQLFEVGFAYQWCSVPTRESSHEGLVTDPHSPARFVYLGTL 784
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Qy      785 SNSRDLRHFQCPVGSPPANPQGLCEVW 811
Db      749 SQFEFGRAFHCPKDSPPNPAHKCSVW 775
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REFERENCE  
AUTHORS  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carminci, P.,  
Komoto, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE  
AUTHORS  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

REFERENCE  
AUTHORS  
5  
The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

JOURNAL  
REFERENCE  
AUTHORS  
6  
(bases 1 to 2496)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carminci, P.,  
Hayashida, K., Hayatsu, N., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kashiwagi, K.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.  
Location/Qualifiers

FEATURES  
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NEIVPAGTILQAPFYAHNHPKALNFGGIGVWGHLELTAFDQGEYDKEGRLPMWQ  
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GEQPLPAVLGNHQLFFVGFQAVLTK"

ORIGIN  
Query Match 47.6%; Score 1606.4; DB 11; Length 2496;  
Best Local Similarity 88.1%; Pred. No. 5.4e-221;  
Matches 1761; Conservative 0; Mismatches 231; Indels 6; Gaps 1;  
QY 377 GGTGGGATTCGAGAGGGGCAAGACAGCTTTAGCTCAGCCAGAGCTGAGCTGGT 436  
DB 292 GGTGGGATTCAGAAAGGACAAAGACACTGTTGGTTCAACACAGTGGAGCTGGT 351  
QY 437 CTTAGCAGGTGCTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496  
DB 352 CTGGAGAGCCCTCATTTCTAGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 411  
QY 497 GGTTCAGTACACAGAGACCCATCCACAGACCTGCTTACAGAGCTTCGATTCGAGT 556  
DB 412 GGT-----CCACAGAGACCCAGCCCATGACCTGCGTCAAGAGCTGCAATTCGAGT 465  
QY 557 GGTGGGAAAAATCTGAGTCTCCCTGAGCCGAGGGGGTGAAGCCCTGAGAGACTTTTACCA 616  
DB 466 AGCTGAAAAATCTGAGTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 525  
QY 617 GTTCTCTGCTGAGGGGCTGAGTTCGAGAGAACCCCTGCTGCTGCTGCTGCTGCTG 676  
DB 526 GTTCTCTGCTGAGGGCTGAGTTCGAGAGAACCCCTGCTGCTGCTGCTGCTGCTG 585  
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QY 737 CACCTTCAACAGCTCTGAGACCAAAACAGGCTATCTGAAGCACCTGCTGAAACAC 796  
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QY 917 AGTAGAGGAGCCTTACAGGGGCCACCCCATTTCTTACCGCTTACATGAGGCCGACTTAA 976  
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QY 977 GAGTTCCAAACAGCAATGTTATCAGGTGAGCAAGTCTGGGCTCTTCTGCGCTCTCGGGA 1036  
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DB 1006 GGAACCTGGGAGTCTGCTGGGTGGGGGCGCCACTTCAAGAGGAGCAGANTGAGAGGAT 1065  
QY 1157 GCTGAGTTGAGATACAGCTGGCCAAATCAAGTGCCTCAGAGCACAGCGGCGCAGCA 1216

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Db      1066 GCTGAGCTGAGATACAGCTGGCTAACATCACTGTGCCCAAGACCAAGGGGTGATGA 1125
Qy      1217 GGAAGAGATTACCAAGATGAGCATTTGGAGCTGCAGGGCTCTGCGCCCTTCATGGA 1276
Db      1126 GGAGAGATTATACAAAGATGAGCATCTCAGAGCTGCAGGGCTCTCGCGCCGCTGGA 1185
Qy      1277 CTGGCTTGAAGTCTGTCTTCTTCTGCTGATCCCATTTGGAGTGAAGTACTGTAGAGCTGT 1336
Db      1186 CTGGCTGAGATCTCTTCTTCTTCTGTTATGCGCATTTGAGTGGGTGATTTCTGAGCTGT 1245
Qy      1337 GGTGTGTATGGAGATGATTATTTGACAGAGTGTCAAGCTCATCAACCGCAAGCAAC 1396
Db      1246 GGTGTGTATGGAGATGATTATTTGACAGAGTGTGTGAGACTCATCAACGTTACTGAGC 1305
Qy      1397 AAGCATCTGAAACATTACTGATCTGGAACCTGTGTCAAAAGAACAACTCTCAAGCTTGA 1456
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Qy      1457 CGGACGCTTGAAGTCTGCAAGAGAGAGCTGTGAGAACCTCTGATGGCACTAAGAGTC 1516
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Db      1486 GGGTTCATCTTGTGAAAGCCACATTTGACCGCAAGAGAAATTCGCGAGGAGAT 1545
Qy      1637 GATCAGGAAATCCGAGCGCATTTGAGAGGCGCTGTGGCAAGCTGTGTTGATGATGA 1696
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Db      1786 CCAAGCTCCGAGAGCTCCAGCGAGAGAGATGATGATGATGATGATGATGATGATG 1845
Qy      1937 CTACTACTTTCCTCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATG 1996
Db      1846 TTAATCTTTCCTCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATG 1905
Qy      1997 CTATGCCCGAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2056
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Db      2026 TCCCTGTGTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2085
Qy      2177 ACAGTACATCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
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Db      2146 AATCATGCCGATATATGAGGAGCTTAAAGCTGCTCAATGCTTAAAGAGATGCTGAG 2205
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Db      2206 AAGCATTTGGGAGAGACAGCCGCTGCTGTGTTGGGCTCAACATCAACAGCTTCTT 2265
Qy      2357 CGTGGATTTGCCCCAGT 2374
Db      2266 CGTGGATTTGCTCAGT 2283

RESULT 2
AK043473
LOCUS
DEFINITION
MUS musculus 7 days neonate cerebellum cDNA, RIKEN full-length
ENZYME-2 homolog [Mus musculus], full insert sequence.
ACCESSION
AK043473
VERSION
AK043473.1 GI:26089750
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
3. Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, D.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
4. The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5. The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6. (bases 1 to 1850)
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

```

## TITLE

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.

## JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

## SOURCE

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/db\_xref="taxon:10090"  
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## ORIGIN

## Query Match

31.4%; Score 1059.4; DB 11; Length 1850;

## Best Local Similarity

86.3%; Pred. No. 1.8e-142;

## Matches 1171;

Conservative 0; Mismatches 186; Indels 0; Gaps 0;

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23 CTGCTCCTCCTCCACATGAACGTGCGCTGCAAGTGGGTGGCGAGGACAGTACCA 82  
519 TCCACAGCACTGCTTACAGAGGCTGATTCGATGCTGGAAGAAATCTGAGATCC 578  
83 GCCCATGACACTGCTGACAGAGCTGATTCGATGCTGGAAGAAATCTGAGATCT 142  
579 CTGACCGAGGGGTGAGCCCTGTGAGAGACTTTTACAGATTCCTGTGGGGCTGAT 638  
143 CTAGACCGTGGGTGAGCCCTGTGAGAGACTTTTACAGATTCCTGTGGGGCTGAT 202  
639 CGAGGAACCCCTGCGGATGGGCTTCTGCTGGAACCTTCAACAGCTCTGGGAC 698  
203 CGAAGAAACCTTACCAATGAGAGCTTCTGCTGGAACCTTCAACAGCTCTGGGAC 262  
699 CAAACAGGCGCATCTGAGAGACTTGTGAAAAACCACTTCACTCAGAGTGA 758  
263 CAGAACAGGCGCATCTGAGAGACTTGTGAAAAACCACTTCACTCAGAGTGA 322  
759 GCTGAGAGAGAGACAGCGCTTCTACCTATCTTGGCTTACAGAGTGGAGCGATGAGAG 818  
323 GCTGAGAGAGAGACTCGAGATTTTACCTGCTGCTTACAGTGGAGCGCATGAGAG 382  
819 CTGGAGCCCAAGCCACTGAGAGACTTACCTAGAGAGTGGTGGTGAACATTTACGGGG 878  
383 CTAGAGACCAAGCCACTTGAAGACTTACCTAGAGAGTGGTGGTGAACATTTACGGGG 442  
879 CCTGGAGACCAAGCACTTATGAGAGTGTGAAGGAGTGAAGGAGGAGCTTACAGGGCC 938  
443 CTTTGGAGACGAGGACAGCTTATGAGAGTGTCTCAAGGAGAGCTTACAGAGGAGCC 502  
939 ACCCATTTCTTACCGCTTACATCAGTGGCGAGCTTGAAGTTCACAGCAATGTTATC 998

503 ACCCCCTTCTTACCGCTTACAGTGGCTGATTCCTAAGATTTCTAAGCAATATCATC 562  
999 CAGGTGACCAAGTGTGGGCTCTTTTCTGCTCTCTGCGGATTTACTTAAACAGATGCC 1058  
563 CAGGTGACCAAGTGTGGGCTCTTTTCTGCTCTCTGCGGATTTACTTAAATGMACTGCC 622  
1059 AATGAAAGTGTCTACCTGCTTATCTGATTTACATGAGGAACTGGGGATGCTGGGT 1118  
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743 GCTTACATCATCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGATTTACCAAGATG 802  
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1299 TTGCTGTCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCTGCTTTC 1358  
863 TTGCTGTCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCTGCTTTC 922  
1359 TTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCTGCTTTC 1418  
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RESULT 3  
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DEFINITION AGENCOURT\_6507206 NIH\_MGC\_124 Homo sapiens cDNA clone IMAGE:5727780  
5', mRNA sequence.  
ACCESSION BM547706  
VERSION BM547706.1 GI:18781705  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1156)



**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 plate: LLAM12722 row: 9 column: 13  
 High quality sequence stop: 650.

**FEATURES**

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 age 27. Library is oligo-dT primed and directionally  
 cloned (EcoRV site is destroyed upon cloning). Average  
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 012."

**ORIGIN**

Query Match 21.2%; Score 714.6; DB 12; Length 1156;  
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 Matches 786; Conservative 0; Mismatches 44; Indels 5; Gaps 4;

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RESULT 4  
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 ACCESSION BU739636  
 VERSION BU739636.1 GI:23678186  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 TITLE 1 (bases 1 to 712)  
 BONDALDO, M.F., LEMMON, G. and SOARES, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PubMed 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: [bento-soares@iowa.edu](mailto:bento-soares@iowa.edu)  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics ([www.resgen.com](http://www.resgen.com)).  
 Seq primer: M13 FORWARD  
 PolA=Yes.

**FEATURES**

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 optic nerve, retina, Retina foveal and Macular, RPS and  
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 /clone\_1b="UI-E-EJ0"  
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 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-E-EJ0 is a subtracted cDNA library constructed  
 according to Bonaldo, Lemmon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested with Notc I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Notc I site and the (dT)<sub>18</sub> tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATCCCGCAT; optic nerve, CCATTAGATG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and choroid, ACCCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NIH).  
TAG\_LIB=UI-B-EJO  
TAG\_TISSUE=Foveal and Macular Retina  
TAG\_SEQ=GTCC"

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Qy	1718	GGAGAAACAGATGCAATGCATCTATGATATGATTTGCCACATTTATCCCTGAGACCCA	1777
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Db	665	GTTGAATTTGTACAACCTTCTCT	686
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DEFINITION	AV708732	ADC Homo sapiens cDNA clone ADCAXE12 5', mRNA sequence.	
ACCESSION	AV708732		
VERSION	AV708732.1	GI:10725997	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 691)		
AUTHORS	Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.		
TITLE	Homo sapiens cDNA ADC clones		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex. 45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.		
FEATURES			
source	location/Qualifiers		
	1..691		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
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	/dev_stage="adult"		
	/lab_host="SOLR"		
	/clone_idb="ADC"		
	/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"		
ORIGIN			
Query Match	19.2%	Score 650;	DB 9; Length 691;
Best Local Similarity	98.1%;	Pred. NO. 1.2e-83;	

Matches	678;	Conservative	0;	Mismatches	11;	Indels	2;	Gaps	2;
OY	2288	ATGCGTGAAGAAAGCATGGGAGAGGACGACAACTCCAGCCGCTGGGGCTCACCAACCA	2347						
Db	1	ATGCGTGAAGAAAGCATGGGAGAGGACGACAACTCCAGCCGCTGGGGCTCACCAACCA	60						
OY	2348	GCTCTTCTGTCGGGAAATTGGCCGAGGATGGGTGCTCGGATCCGACACACAGAGGCTCTCA	2407						
Db	61	GCTCTTCTGTCGGGAAATTGGCCGAGGATGGGTGCTCGGATCCGACACACAGAGGCTCTCA	120						
OY	2408	CGAGGGGCTGGTGACCCGACCCCAACACCCTGCACCGCTTCGACGTGGCACTCTCTC	2467						
Db	121	CGAGGGGCTGGTGACCCGACCCCAACACCCTGCACCGCTTCGACGTGGCACTCTCTC	180						
OY	2468	CAACTCCCGTGACTTCTCGTGGGCACTTCGCTGCTCTGTGGGCTCCCCCATGAACCAAG	2527						
Db	181	CAACTCCCGTGACTTCTCGTGGGCACTTCGCTGCTCTGTGGGCTCCCCCATGAACCAAG	240						
OY	2528	GCACCTGTGAGAGGT	2587						
Db	241	GCACCTGTGAGAGGT	300						
OY	2588	CTGGGGGAGGCTCTCTCTGACAAAGCTGTTTGTCTTGGGTTTGGAGAAAGCAATGCAAGC	2647						
Db	301	CTGGGGGAGGCTCTCTCTGACAAAGCTGTTTGTCTTGGGTTTGGAGAAAGCAATGCAAGC	360						
OY	2648	TGGGCTGGGCTCTAGTCCCTCCGCCCAAGGTGACATGAGTACAGACCCTCTCAATCAC	2707						
Db	361	TGGGCTGGGCTCTAGTCCCTCCGCCCAAGGTGACATGAGTACAGACCCTCTCAATCAC	420						
OY	2708	CACATTGTGCTCTGCTCTTTGGGGGTGGCCCTGCTCCAGCAGAGCCCCCAACATTCAC	2767						
Db	421	CACATTGTGCTCTGCTCTTTGGGGGTGGCCCTGCTCCAGCAGAGCCCCCAACATTCAC	480						
OY	2768	TGACATCTTTCCGATGACACCCTGCTGAGAAAGGCTGGGGTGGAGGAGGACAGTCCCATTA	2827						
Db	481	TGACATCTTTCCGATGACACCCTGCTGAGAAAGGCTGGGGTGGAGGAGGACAGTCCCATTA	540						
OY	2828	GGAAGAGATGCTGCTCTTCTGTCTCCCAAGGCTCACTAGCTGGCGGACATGGGGCTTGC	2887						
Db	541	GGAAGAGATGCTGCTCTTCTGTCTCCCAAGGCTCACTAGCTGGCGGACATGGGGCTTGC	599						
OY	2888	GTCGCTGCCCCACTGTGACCCACAGGCTTGGGTGTGTACTTCTTGACATTCTCCCAAG	2947						
Db	600	GTCGCTGCCCCACTGTGACCCACAGGCTTGGGTGTGTACTTCTTGACATTCTCCCAAG	658						
OY	2948	CTCACTCAATGTCGACCTTGAAGGGGTGACCTA 2978							
Db	659	CTTACTCAATGTCGACCTTGAAGGGGTGACCTA 689							

[illegible]



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Db      1 GGAAGAGATATACACAGATGAGCATTGTGGAGCTGCAAGCTCTGCGCCCTCCATGGA 60
QY      1277 CTGGCTTGAAGTCTCTGCTCTTCTTCTGCTGTACCAATTTGAGTGAAGTCTGAGCTGT 1336
Db      61 CTGGCTTGAAGTCTCTGCTCTTCTTCTGCTGTACCAATTTGAGTGAAGTCTGAGCTGT 120
QY      1337 GGTGTGTATGGATGATTAATTTGAGAGAGTGTCAAGCTCATCAACCGCAGGAGC 1396
Db      121 GGTGTGTATGGATGATTAATTTGAGAGAGTGTCAAGCTCATCAACCGCAGGAGC 180
QY      1397 AACCATCTGCAACAATTTACCTGATCTGGAACCTGTGTCAAAAGACAACCTCAAGCTCTGA 1456
Db      181 AACCATCTGCAACAATTTACCTGATCTGGAACCTGTGTCAAAAGACAACCTCAAGCTCTGA 240
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QY      1637 GATCAGGGAATTCGACCGCATTTTGAAGAGCCCTGTGAGACAGCTGTGTTGATGATGA 1696
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Db      481 GAAGACCCCGCAGGAGGCAAGAGAAAGAGATGCATATGATATGATGATGATGATGATGATG 540
QY      1757 AGACTTATCTGAGAGCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 1816
Db      541 AGACTTATCTGAGAGCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 600
QY      1817 AGATCTTTCTTCCAAACATG 1838
Db      601 AGATCTTTCTTCCAAACATG 622

RESULT 9
LOCUS   BM713622
DEFINITION
UI-B-EJ0-aho-n-24-0-UI.r1 UI-B-EJ0 Homo sapiens cDNA clone
UI-B-EJ0-aho-n-24-0-UI 5', mRNA sequence.
ACCESSION
BM713622.1 GI:19026880
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Bukayocia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 596)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
97044477
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: Bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.regen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 596

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optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
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/lab_host="PH108 (life Technologies) (T1 phage resistant)"
/clone_1lb="UI-B-EJ0"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
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UI-B-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATTCAGAG; lens, CGATTAGAG; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGAG; retina, CCGGAG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

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## ORIGIN

Query Match 17.5%; Score 592.4; DB 12; Length 596;  
 Best Local Similarity 99.5%; Pred. No. 2.2e-75;  
 Matches 593; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2375 GTGTGTCTGTGTGCGGACGACACGAGAGCTCTACGAGGGGCTGTACCGACCCCAACG 2434
Db      61 GTGTGTCTGTGTGCGGACGACACGAGAGCTCTACGAGGGGCTGTACCGACCCCAACG 120
QY      2435 CCCTGCCGCTTCCGCGTCTGGGCACTCTTCCAACTCCCGTGAATTTCTGCGGCACTT 2494
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QY      2495 CCGCTGCGCTGTGCGCTCCCGCATGAAACCGAGGAGCTGTGTGAGTGTGTAGACTTG 2554
Db      181 CCGCTGCGCTGTGCGCTCCCGCATGAAACCGAGGAGCTGTGTGAGTGTGTAGACTTG 240
QY      2555 GATCAGGGGAGAAATTCCTGCTGTACAGAGCTTGGGCACTCTCTCTGACAAACTGT 2614
Db      241 GATCAGGGGAGAAATTCCTGCTGTACAGAGCTTGGGCACTCTCTCTGACAAACTGT 300
QY      2615 TTGCTCTTGGGTTGGAGAGAAATGCAAGCTGGGCTGTGTGCTCTCTCTCTCTCTCTCT 2674
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Db 481 GAAGAGGTCTGGGTGGGAGGCGCAGTTCACATAGAAAGAGTGCCTCTTGTGTCNCCA 540

QY 2855 GGCTCACTCAAGCTTGGCGGCGCATATGGGCGCTGCGCTGCTGCTCCCACTGTGACCCAC 2910

Db 541 GGCTCACTCAAGCTTGGCGGCGCATATGGGCGCTGCGCTGCTGCTCCCACTGTGACCCAC 596

RESULT 10

CB519920 704 bp mRNA linear EST 09-JUL-2003

LOCUS UI-M-G10-cek-e-23-0-UI.r1 NIH\_BMAP\_G10 Mus musculus cDNA clone

DEFINITION IMAGE:6840672 5', mRNA sequence.

ACCESSION CB519920

VERSION CB519920.1 GI:29353275

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 704)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE Unpublished (1999)

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [rgabbs-remail.nih.gov](mailto:rgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES

source

Location/Qualifiers

1..704

/organism="Mus musculus"

/mol\_type="mRNA"

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/db\_xref="taxon:10090"

/clone="IMAGE:6840672"

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/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_1lb="NIH BMAP G10"

/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the Polysa tail Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 17.1%; Score 578.8; DB 14; Length 704;

Best Local Similarity 86.8%; Pred. No. 1.9e-73;

Matches 625; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1396 CAAGCATCTGGAACAATTACCTGATCTGGAACCTGTGCAAAAGACAACCTCAAGCTGG 1455

Db 1 CAGGCAATCTGACAAATTAATTAATTGGAACCTGTGACAGAGACCACTCAAGCTTG 60

QY 1456 ACCGAGCCTTTAGCTTGACACAGAGAGCTGTGAGACCTCTTATGGAAGT 1515

Db 61 ACCAGCCTTTGAGACTGACAGAGAAATGTGTGAGAGACCTCTTACGATACCAAGAGT 120

QY 1516 CCTGTGTGCGGAGGTGGGAGACCTGATCTCCAAACGAGATGACGCCCTTGGCTTGTGCTT 1575

Db 121 CCTGCACTCGAGGTGGGAGACCTGATCTCCAAATACAGATATAGCTTGGCTTGTGCTT 180

QY 1576 TGGGGTCCCTCTTGTGAAAGCCACGTTTACCGGCAAGCAAAATTTGACAGGGGA 1635

Db 181 TGGGTTCATCTTTGTGAAAGCCACATTTGACCGCAAGCAAGAAATTCGCCAGGGGA 240

QY 1636 TGATCAGCAAAATCCGAGACCGCATTTGAGAGAGCCCTGGGACAGCTGGTTTGGATGGATG 1695

Db 241 TGATCAATATAATCCGCTCTGCTTTGAGAGACACCTGGGACACTTGTGTAATGGATG 300

QY 1696 AGAAGACCCGCGCAGGACGAGCAAGAGAAAGAGATGSCATCTATGATATGATGGTTTCC 1755

Db 301 AGAAGACCCGCGCTGGAGCGCAAGCAAGAGAAAGAGATGSCATCTATGATATGATGGTTTCC 360

QY 1756 CAGACTTTATCTGTGAGCCCAAGAGCTGATGATGATTTATGACGGGTAAGAAATTTCTG 1815

Db 361 CTGATTTATCTGTGAGCCCAAGAGCTGATGATGATTTATGATGAGGATGAAATCTCTG 420

QY 1816 AAGATTTCTTTTCCAAACATGTTGAATTTGTACAATCTTCTGCAAGTTATGGCTG 1875

Db 421 AAGATTTCTTTTCCAAACATGTTGAATCTGTACAACTTCAGCTAAGGATGGCTG 480

QY 1876 ACCAGCTCGCAAGCCTCCGAGCGGACAGCATGAGCATGCCCGCAGACATGATG 1935

Db 481 ACCAGCTCGCAAGCCTCCGAGCGGACAGCATGAGCATGCCCGCAGACATGATG 540

QY 1936 CCTACTACCTTCCAACTAAGATGATGATGTTTCCCGCTGGCATCTTGCAGGCCCTCT 1995

Db 541 CTACTACCTTCCAACTAAGATGATGATGTTTCCCGCTGGCATCTTGCAGGCCCTCT 600

QY 1996 TCTATGCCCGCAACCAACCCCAAGCCCTGAACTTCGTGGCATCGGTGTCATGAGGGCC 2055

Db 601 TCTATGCTCAACAACATTCAGAGGCTTGAACCTTGTGTGATCGCGATGATGATGAGG 660

QY 2056 ATGAGTTGACGATGCTTGTGATGACCAAGGCGCGCATGATGAC 2099

Db 661 ATGAGTTGACGATGCTTGTGATGACCAAGGCGCGCATGATGATGAC 704

RESULT 11

AU296410 651 bp mRNA linear EST 17-JUL-2003

LOCUS AU296410 full-length enriched pig cDNA library, main and accessory

DEFINITION Olfactory bulb Sus scrofa cDNA clone olf\_101\_A12 5', mRNA sequence.

ACCESSION AU296410

VERSION AU296410.1 GI:32948973

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 651)

AUTHORS Fujisaki,S., Hiraiwa,H., Eguchi,T., Watanabe,Y., Honma,D., Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

TITLE Construction of a full-length library of swine olfactory bulb and its preliminary characterization

JOURNAL Unpublished (2003)

COMMENT Contact: Seiichiro Fujisaki  
Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Kunitzaki, Inashiki, Ibaraki 305-0901, Japan  
Tel: 81-298-38-8659  
Fax: 81-298-38-8659  
Email: [seifuji@affrc.go.jp](mailto:seifuji@affrc.go.jp).

FEATURES

source

1..651

/organism="Sus scrofa"

/mol\_type="mRNA"

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/clone="OLF\_101\_A12"





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 Db 601 CCCCCATG 608

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 DEFINITION 602391085F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4502901 5',  
 mRNA sequence.  
 BG294032  
 BG294032.1 GI:13054261  
 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 856)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Found through the I.M.A.G.E. Consortium/LIML at:  
 http://image.llnl.gov  
 plate: LIML0372 row: 3 column: 22  
 High quality sequence, stop: 717.  
 Location/Qualifiers  
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 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 15.4%; Score 521.4; DB 12; Length 856;  
 Best Local Similarity 81.1%; Pred. No. 3.2e-65;  
 Matches 656; Conservative 0; Mismatches 146; Indels 7; Gaps 4;

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 1 AGTTCTAACGACATATCATCCAGGTGACCAAGTCTGGCTTTTCTGCCCTCGAGAT 60

Db 1038 TACTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCTTATCTGATTACATGAG 1097  
 61 TACTACTTAAATGAACTGCCAATGAGAAAGTCTCACTGCTTATCTGATTACATGAGT 120

QY 1098 GAACTGGGAGTGCCTGGGTGGGGGGCCCACTCCACAGAGGAGAGATGACAGAGT 1156  
 121 GAGCTGGGAGTGCCTGGGTGGGGGGCCCACTCCACAGAGGAGAGATGACAGAGT 180

Db 1157 GCTGAGTTGAGATACAGCTGGCCCAATCATCAGTCCCAAGAGCCAGGCGCGACGA 1216  
 181 GCTGAGCTGAGATACAGCTGGGTAACTACATCTGTCCTCCAGAGCCAGGCGGTATGA 240

QY 1217 GAGAGATCTTACACAGATGAGCAATTTGGAGCTGCAAGGCTCTGGCGCCCTTCATGA 1276  
 241 GAGAGATCTTATCACAAGATGAGCAATCTGAGAGCTCAGGCTCTCGCGCCCGCGTGA 300

QY 1277 CTGGCTTGAATCTCTGTTCTTTCTTGCTGTCACCATTTGAGTTGAGTCTGACCTGT 1336  
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 Db 301 CTGGCTTGAATCTCTTCTTTCTTTGTTATGCGCATTTGAGTTGGGTGATTCGACCTGT 360

QY 1337 GGTGTGTATGAGATGATTTATTTGACAGAGGTGTCAAGCTCATCAACGACGAGAC 1396  
 361 GGTGTGTATGAGATGATTTATTTGACAGAGGTGTCAAGCTCATCAACGAGTCAAGACC 420

QY 1397 AACGATCTTGAAACATTTACTCTGATCTGGAACCTGTGTGAAAGACAACTTAAGCTGGA 1456  
 421 AACGATCTTGAAACATTTACTCTGATCTGGAACCTGTGTGAAAGACAACTTAAGCTTGA 480

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 481 CCGAGCTTTGAGTCTGACACAGAGAGTGTGTGAGACCTCTTATGACATTAAGAGTCT 540

QY 1517 CTGTGTGCGAGAGTGTGACAGCTGCAATCTTCAACAGAGTACGCCCTTTGCTTTGCTTT 1576  
 541 CTGTGTGCGAGAGTGTGACAGCTGCAATCTTCAACAGAGTACGCCCTTTGCTTTGCTTTG 600

QY 1577 GGGGTCC--CTCTGCTGAAAGGCCAGCTTTGACCGG--CAAGCAAGAAATGACAGAG 1632  
 601 GGTTCACACTTTTGTGAAAGCCACATTTTGAACGACAAAGAAATGACCGAGAG 660

QY 1633 GGATGATCAGCAAAATCCGACCGCATTTGAGAGGCGCTGGAGACGTGTTGGATAG 1692  
 661 GGATGATCAGCAAAATCCGACCGCATTTGAGAGGCGCTGGAGACGTGTTGGATAGT 720

QY 1693 ATGAGAAAGCCGCGCAGGACGCC--AAGGAGAAAGCATGTCATGATGATGATTTGG 1750  
 721 TGCAAAAGACCGGGGTGGAGCCCAAGGAGAAAGCGATGTCATGATGATGATGACG 780

QY 1751 TTTCCAGACTTATCTGAGGCCCAAG 1779  
 781 GGTACCGGATTCATCTGAAGGCCAGAG 809

RESULT 14  
 LOCUS BY718681 626 bp mRNA linear EST 17-DEC-2002  
 DEFINITION Mus musculus full-length enriched, adult male medulla oblongata  
 BY718681  
 BY718681.1 GI:27131798  
 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 626)  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bone, H., Kondo, S.,  
 Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schombach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bull, C.,  
 Hume, D.A., Quackenbush, J., Schmitt, L.M., Kanaphan, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.M., Bratt, D., Brusic, V.,  
 Chordia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
 Fletcher, C.F., Forrest, A., Prager, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Muralis, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Perea, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, U.V., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sanderlin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takekura, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Mahlestedt, C., Wang, Y., Matanabe, Y.,  
 Wells, C., Wilming, L.G., Wyshak-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,  
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,





This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.

This clone (DKFZp761M0913) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source

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1..533
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp761M0913"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="761 (synonym: hamy2)"
/ncore="Vector: pSport1; Site_1: NotI; Site_2: SalI"
```

## ORIGIN

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Query Match      14.8%; Score 500.4; DB 9; Length 533;
Best Local Similarity 97.9%; Pred. No. 3.6e-62;
Matches 507; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 360 CTCTGCTTGAAGACTATGATGGGATTCAGAGGGGACAAAGACAGCTGTAGGCTCAGC 419
    |||
Db 16 CTGGAGCTGGCAGCAAGTCGGATTCAGAGGGGACAAAGACAGCTGTAGGCTCAGC 75
    |||

QY 420 ACCGAGCTGAGGCTGCTTAGCAGGCTCTCTACTAGTGTGCTGCACTGCTTCTGGC 479
    |||
Db 76 ACCGAGCTGAGGCTGCTTAGCAGGCTCTCTACTAGTGTGCTGCACTGCTTCTGGC 135
    |||

QY 480 TGCTTGTGCCCCCTAGGGGCTCAGTACACAGAGACCATCCACAGCACTGCTTACA 539
    |||
Db 136 TGCTTGTGCCCCCTAGGGGCTCAGTACACAGAGACCATCCACAGCACTGCTTACA 195
    |||

QY 540 GAGGCTGCAATTCAGTGGCTGGAAAAATCCTGAGTCCCTGACCGAGGGGTGAGCCC 599
    |||
Db 196 GAGGCTGCAATTCAGTGGCTGGAAAAATCCTGAGTCCCTGACCGAGGGGTGAGCCC 255
    |||

QY 600 TGTGAGGACTTTTACCAAGTCTCCTGTGGGGGCTGAGTTGGAGGAACCCCTGCCCGAT 659
    |||
Db 256 TGTGAGGACTTTTACCAAGTCTCCTGTGGGGGCTGAGTTGGAGGAACCCCTGCCCGAT 315
    |||

QY 660 GGGGCTCTGCTGGAACACCTTCAACAGGCTTGGAGCCAAAACAGGCCATATGTAAG 719
    |||
Db 316 GGGGCTCTGCTGGAACACCTTCAACAGGCTTGGAGCCAAAACAGGCCATATGTAAG 375
    |||

QY 720 CACCTGCTTGAACACCACTTCACTCCAGCAGTGAAGTGAAGCAAGACAGAGCC 779
    |||
Db 376 CACCTGCTTGAACACCACTTCACTCCAGCAGTGAAGTGAAGCAAGACAGAGCC 435
    |||

QY 780 TTCTAGCTATCTTGGCTTACAGGTGAGGCAATTGAGAGCTGGAGCCCAAGCACTGGA 839
    |||
Db 436 TTCTAGCTATCTTGGCTTACAGGTGAGGCAATTGAGAGCTGGAGCCCAAGCACTGGA 495
    |||

QY 840 GACCTCATTTGAGAGATTGGTGTGTTGGAACATTACGGG 877
    |||
Db 496 GACCTCATTTGAGAGATTGGTGTGTTGGAACATTACGGG 533
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Search completed: July 3, 2004, 13:01:58  
Job time : 8128 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 20:05:51 ; Search time 26 Seconds  
(without alignments)  
3000.436 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSPPMNPQLCEWV 811

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3662	85.5	825	2	endothelin convert
2	2592.5	60.6	770	2	endothelin convert
3	2586.5	60.4	754	2	endothelin convert
4	2567.5	60.0	754	2	endothelin convert
5	2561	59.8	758	2	endothelin convert
6	2546	59.5	758	2	endothelin convert
7	1440	33.6	774	2	endothelin convert
8	1282.5	30.0	750	1	neprilysin (EC 3.4
9	1272.5	29.7	750	1	neprilysin (EC 3.4
10	1272	29.7	751	1	neprilysin (EC 3.4
11	1199.5	28.0	766	2	neprilysin (EC 3.4
12	1192.5	27.9	750	2	neprilysin (EC 3.4
13	1122.5	26.2	590	2	neprilysin (EC 3.4
14	994.5	23.2	769	2	neprilysin (EC 3.4
15	958.5	22.4	732	1	neprilysin (EC 3.4
16	937	21.9	754	2	neprilysin (EC 3.4
17	892	20.8	700	2	neprilysin (EC 3.4
18	878.5	20.5	706	2	neprilysin (EC 3.4
19	760	17.8	667	2	neprilysin (EC 3.4
20	758.5	17.7	663	2	neprilysin (EC 3.4
21	747	17.4	663	2	neprilysin (EC 3.4
22	673.5	15.7	823	2	neprilysin (EC 3.4
23	614	14.3	798	2	neprilysin (EC 3.4
24	590.5	13.8	801	2	neprilysin (EC 3.4
25	562.5	13.1	630	2	neprilysin (EC 3.4
26	561.5	13.1	630	2	neprilysin (EC 3.4
27	550	12.8	627	2	neprilysin (EC 3.4
28	549	12.8	627	2	neprilysin (EC 3.4
29	545	12.7	627	2	neprilysin (EC 3.4

30	513	12.0	564	2	probable zinc meta
31	510	11.9	726	2	protein F18A12.1
32	506.5	11.8	774	2	hypothetical prote
33	457.5	10.7	649	2	protein F18A12.6
34	375	8.8	732	2	hypothetical prote
35	366.5	8.6	651	2	hypothetical prote
36	349	8.2	658	2	hypothetical prote
37	341	8.0	534	2	hypothetical prote
38	330.5	7.7	570	2	protein F18A12.3
39	315	7.4	684	2	hypothetical prote
40	294	6.9	734	2	protein F18A12.4
41	225.5	5.3	817	2	hypothetical prote
42	176.5	4.1	550	2	protein F18A12.5
43	172.5	4.0	198	2	protein T06D4.5
44	172.5	4.0	198	2	hypothetical prote
45	148.5	3.5	491	2	hypothetical prote

## ALIGNMENTS

## RESULT 1

146078  
endothelin converting enzyme (EC 3.4.24.-) 2 - bovine (fragment)  
C/Spectrum: Bos primigenius taurus (cattle)  
C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #ext\_change 20-Sep-1999  
C/Accession: 146078

R/Emoto, N.; Yanagisawa, M.

J. Biol. Chem. 270, 15262-15268, 1995

A/Title: Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-sensitive me

A/Reference number: A57042; MUID:95318093; PMID:7797512

A/Accession: 146078

A/status: preliminary; translated from GB/EMBL/DBJ

A/molecule type: mRNA

A/residues: 1-825 <EMO>

A/cross-references: EMBL:U27341; NID:9897599; PID:9897600

A/genetic:

A/gene: BCE-2

A/superfamily: neprilysin

C/keywords: hydrolase; metalloproteinase

Query Match	Score	Match	Length	ID	Description
Best Local Similarity	93.0%	Pred. No. 2,7e-241;			
Matches	690;	Conservative	22;	Mismatches	28;
				Indels	2;
				Gaps	1;
QY	70	WRYTCHPLHSISGLCSRTWVGQKGTROLGSRTOLEVLTAASLLALMLGCTVALGV	129		
DB	86	WTVSSRGVATVQVINE--AGFRKRTSRLLGHTOLEVLTAAGVSLALMLGCTVALGV	143		
QY	130	OYHRDPSHTCLTEACIRVAGKILSLDGVSPCEDFYQFSGCGMIRRPPLDGRGRWNT	189		
DB	144	OYHRDPSHTCLTEACIRVAGKILSLDGVSPCEDFYQFSGCGMIRRPPLDGRGRWNT	203		
QY	190	FNSLWDONALIKHLENTFNSSSEAEQKORFYLSCLQVERIEELGAQPLRLIEKIG	249		
DB	204	SNSLWDONALIKHLENTFNSSSEAEKQKORFYLSCLQVERIEELGAHRLDLKIG	263		
QY	250	GNITGPMQDNFMELKAVAGTYRATPFTYIISADSSNSNYIYQVQSGFLPSPRY	309		
DB	264	GNITGPMQDNFMELKAVAGTYRATPFTYIISADSSNSNYIYQVQSGFLPSPRY	323		
QY	310	YANRTANEKVLTAAYLDYMEELGMLGGRPTSRQOQVLELEIOLANTTVPODORDE	369		
DB	324	YANRTANEKVLTAAYLDYMEELGMLGGRPTSRQOQVLELEIOLANTTVPODORDE	383		
QY	370	KYHKMSISELQALAPSDMTEFLSLPELSDSEPVVYVGMVYLQGVSELINRTES	429		
DB	384	KYHKMSIAELQALAPSDMTEFLSLPELSDSEPVVYVGMVYLQGVSELINRTES	443		
QY	430	ILANTYILNVLVOKTSSLDPRFSAOEKLETLVGTGKSCVRRNOTCISNTDAGFALG	489		
DB	444	ILANTYILNVLVOKTSSLDPRFSAOEKLETLVGTGKSCVRRNOTCISNTDAGFALG	503		

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Db      50 HSPSGRCW-----AATQVEKRLVVLVLAAGL 80
QY      121 LGCIVALGVQYTH -RDESHSTCLTFACIRVAGKILIESLDKRGVSCEDPEYQGS CGGMIRMP 179
Db      81 VACIAAAGIYQYTRSP--SVCLSEACVSVTSILSSMDPVDDCHPFFSYACCGMIKAMP 138
QY      180 LPDGRSMRNPNSIMWDNOAAILKHLIENTFNSSSEAECKTORFYSLCQVERIEELGAQ 239
Db      139 VPDHSHWGTGTSNIMENHOAIKHLIENTST-ASVSEKERRAQQYTRACMETHTIEELIRAK 197
QY      240 PLRDLIEIKGGMNITGMPDODNFMEVLEKAAAGYTRAPPEFTVYISADSKSNSNVIOVDQ 299
Db      198 PLMLIERLGRKMTITGMAKDNFQDTIQVTAHRTSPFSVYVSADSKSNSNVIOVDQ 257
QY      300 SGLELPSRDYYLYNLTANAEKYLTAYLDMELGMLL -GGRPTSTREMOQVLELEIQLIANT 358
Db      258 SGLELPSRDYYLYNLTANAEKYLTAYLDMVQLGKLLGGGDEBAIRPQMQLILDEPTALANI 317
QY      359 TVPDQDRRDEEKIYHKRSISELOALAPSMQMLEFLSLSPLELSDSSEPPVYVYGMDFYLOQ 418
Db      318 TIPEKRRDEELIYHKTAABELQTLAPAIMWLPPLANTIPYVVEINSEBEPITVVDKEXYLEQ 377
QY      419 VSELIINTEBESILNNYLIANLYVQKTTSSLDRRPESAEKLELTLYGFKKSCVPRMQCIS 478

```

Db	438	DTENNIGFALGPMFVKATPAEDSKSIATTEILLETKKAFESLSLTLMKMEDESTRKSAEKA	497
Qy	539	DAIYDMIGPEPTELEPEKELDDVVDYGEISDSFQFOMLNIYNFSAXYMAOOLRPERDQ	598
Db	498	DAITNMIGYFPEFINDPEKELDVFENDYTAVPDLYTENAMREFNSMRRTAOOLKKAPRNDQ	557
Qy	599	WSMTPTQVNAVAYLTETKNEIVFPAGIIOAPFYARNHPKALNFGGIGVVMGHELTTHAPDDG	658
Db	558	WSMTPTPMVNAVAYSTPTKNEIVFPAGIIOAPFYTRSSPALNFGGIGVVMGHELTTHAPDDGQ	617
Qy	659	REYDEKGNLRPMMWONESLAAFRNHTACMEEOYNOYQNGSERLNGRQTIGENIADNGGLKA	718
Db	618	REYDNGGNLRPMMWONSSVFEAKFRQTECMVQDSYNSVNGEPVNGRHTLGENIADNGGLKA	677
Qy	719	AYNAYKAMLRKHGEEOQLPAVGLTNHOLFVPGPAQWCSVTRPSSSHEGLVTPDHSARF	778
Db	678	AYRYAYQWVWKKNGAGHSLPTLGLTNNOOLFVGFGEQWCSVTRPSSSHEGLITDPSHSRF	737

## 2

RESULT 3  
A53679  
endothelin converting enzyme (EC 3.4.24.-) - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 20-Jun-2000  
C.Accession: A53679; U00189  
R.Shimada, K.; Takahashi, M.; Tanzawa, K.  
J. Biol. Chem. 269, 18275-18278, 1994  
A.Title: Cloning and functional expression of endothelin-converting enzyme from rat endo  
A.Reference number: A53679; MUID:94308046; PMID:8034569  
A.Accession: A53679

A:Molecule type: mRNA  
A:Residues: 1-754 <SH>  
A:Cross-references: GB:D29683; NID:G529084; PIDN:BA06152.1; PID:G529085  
C:Superfamily: neprilysin  
C:Keywords: glycoprotein, hydrolase; metalloproteinase; transmembrane protein; zinc  
F:1-52/Domain: intracellular #status predicted <INT>  
F:53-73/Domain: transmembrane #status predicted <TM>  
F:74-754/Domain: extracellular #status predicted <EXT>  
F:125/Binding site: substrate (Arg) #status predicted  
F:150,171,194,254,300,346,357,523,616,635/Binding site: carbohydrate (Asn) (covalent) #

F:591.595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

Query Match 60.4%; Score 2586.5; DB 2; Length 754;

Best Local Similarity 59.9%; Pred. No. 4.6e-168; Matches 479; Conservative 122; Mismatches 151; Indels 47; Gaps 5;

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14 MVEYKATLDEDEAPETPEVGASPDAMEVKGKSPSPSPGMPGTGTPRSSGLFMRVT 73
2 MSYKATLDEDELDVLSBGDYVPNGLQVNF-----RSRSQGRCH--- 43
74 CPHLSISGLCSRTWVGFKGTROLGSRTOLEVLVAGSLLLAALLGLVALGVGYR 133
44 -----AARTSEKRLVVLVTLAAGLVACLAAGLGIQY-R 76
134 DPHSHSTCLTEACIRVACKLIESLDKGVSPCEDFYQSCGGMIRNPLPDGRSMNTNSL 133
77 TRTPVCLTEACVSVSSILNSMDPTVPCODFFSVACGWMIRANPVDPDGRSMGTFTSNL 136
194 WDNQNALIKHLLENTFNSSEBAOKTORFYLSCLOVERIEELGAOPLRLIEKIGGMI 253
137 WEINQALIKHLLENST-ASASEAKKAQVYVRACMETRIEELRAKPLMELIEKLGMI 135
254 TGEWODNMEVLAAGVYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYVYLR 313
196 TGEWAKDNFQDTLOVTAHYRTSPFESVYVSADSKSSNSNVIOVDSGLFLPSRDYVYLR 255
314 TANBKVLTAIDYMEBELGMLL-CGRPTSTEQMOQVLELEIOLANTVPODORDEEK 372
256 TENBKVLTAIDYMEBELGMLL-CGRPTSTEQMOQVLELEIOLANTVPODORDEEK 315
373 HKMSISELOALAPMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPBILN 432
316 HKTAELQTLAIAINMLPFLNAILFYVEINSEPIVYKELRYOVTILNSTDKCLN 375
433 NYLIMLVOKTSSLDKRRFESSAOKLETLVGTKSCVPRMOTCISNTDAGLFGALSG 492
376 NYMMMLVVKRTSFLDQRFQDADKEFMEVMTGKTKCLPRMKFCVSDTENNLGFGALG 435
493 VKATPDRQSKELAEGLMSEIRTAPEEALGOLVWMDKTRQAKAKADAIYDMIGPDP 552
436 VKATPDRQSKELAEGLMSEIRTAPEEALGOLVWMDKTRQAKAKADAIYDMIGPDP 495
553 EPEKELDYVDGYEISEDSFFQNMNLNYPFSAKYMADOLRKPSRDQSMPTPOTVNAVYLR 612
496 DPEKELDYVDGYEISEDSFFQNMNLNYPFSAKYMADOLRKPSRDQSMPTPOTVNAVYLR 555
613 TKNEIVFPAAGILQAPFYARNHPKALNFGGIGVWGHGLTHAFDQGREYDKEGSLRPMWQ 672
556 TKNEIVFPAAGILQAPFYARNHPKALNFGGIGVWGHGLTHAFDQGREYDKEGSLRPMWQ 615
673 NBSLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGIKAAVYNAKYLKRGHE 732
616 NSSVEAFKQGTACVBEQVYNGVNGEVRNGHRTLGENIADNGIKAAVYNAKYLKRGHE 675
733 EQLPPLVGLTNNHQLFVGFAGVWCVSTPSSHEGLVTDHSPARFVYGLTSLNSRDEL 792
676 EQLPPLVGLTNNHQLFVGFAGVWCVSTPSSHEGLVTDHSPARFVYGLTSLNSRDEL 735
793 HFGCPVGSPPMNPQGLCEVW 811
736 HFGCPVGSPPMNPQGLCEVW 754
```

RESULT 4  
S47268  
endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:Accession: S51010; S47268  
R:Schmidt, M.; Kroege, B.; Jacob, E.; Seuburger, H.; Subkowski, T.; Otter, R.; Meyer,  
FBS Lett. 356, 238-243, 1994  
A>Title: Molecular characterization of human and bovine endothelin converting enzyme (EC

A:Reference number: S51009; MWID:95104423; PMID:7805846  
A:Accession: S51010  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <SC2>  
A:Cross-references: EMBL:Z5306; NID:9535074; PIDN:CAA84547.1; PID:9535075  
C:Superfamily: neprilysin  
C:Keywords: hydrolase; metalloprotease; zinc  
F:591.595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

Query Match 60.0%; Score 2567.5; DB 2; Length 754;

Best Local Similarity 59.6%; Pred. No. 9.2e-167; Matches 477; Conservative 119; Mismatches 154; Indels 51; Gaps 7;

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14 MVEYKATLDEDEAPETPEVGASPDAMEVG-KGASPFSPGSPGMPGTGTPRSSGLFMRV 72
2 MSYKATLDEDELDVLSBGDYVPNHLDVNFNG-----PRNGRCW--- 43
73 CPHLSISGLCSRTWVGFKGTROLGSRTOLEVLVAGSLLLAALLGLVALGVGYR 132
44 -----AARTSEKRLVVLVTLAAGLVACLAAGLGIQY 76
133 -RDPHSTCLTEACIRVACKLIESLDKGVSPCEDFYQSCGGMIRNPLPDGRSMNTNSL 191
77 TRTP--SVCLSEACISVTSILNSMDPTVPCODFFTVACGWMIRANPVDPDGRSMGTFTSNL 134
192 SLMDQNALIKHLLENTFNSSEBAOKTORFYLSCLOVERIEELGAOPLRLIEKIGGMI 251
135 NMENQALIKHLLENST-ASVSEAKKQVYVRACMETRIEELRAKPLMELIEKLGMI 193
252 NITGPMODNMEVLAAGVYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYVYLR 311
194 NITGPMODNMEVLAAGVYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYVYLR 253
312 NITANEKVLTAIDYMEBELGMLL-CGRPTSTEQMOQVLELEIOLANTVPODORDEEK 370
254 NITANEKVLTAIDYMEBELGMLL-CGRPTSTEQMOQVLELEIOLANTVPODORDEEK 313
371 IYHKMSISELOALAPMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPBILN 430
314 IYHKMSISELOALAPMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPBILN 373
431 LNNYIMLVOKTSSLDKRRFESSAOKLETLVGTKSCVPRMOTCISNTDAGLFGALSG 490
374 LNNYIMLVOKTSSLDKRRFESSAOKLETLVGTKSCVPRMOTCISNTDAGLFGALSG 433
491 LEVKATPDRQSKELAEGLMSEIRTAPEEALGOLVWMDKTRQAKAKADAIYDMIGPDP 550
434 LEVKATPDRQSKELAEGLMSEIRTAPEEALGOLVWMDKTRQAKAKADAIYDMIGPDP 493
551 ILEPEKELDYVDGYEISEDSFFQNMNLNYPFSAKYMADOLRKPSRDQSMPTPOTVNAVYLR 610
494 ILEPEKELDYVDGYEISEDSFFQNMNLNYPFSAKYMADOLRKPSRDQSMPTPOTVNAVYLR 553
611 LPTKNEIVFPAAGILQAPFYARNHPKALNFGGIGVWGHGLTHAFDQGREYDKEGSLRPMWQ 670
554 LPTKNEIVFPAAGILQAPFYARNHPKALNFGGIGVWGHGLTHAFDQGREYDKEGSLRPMWQ 613
671 WDNQNALIKHLLENTFNSSEBAOKTORFYLSCLOVERIEELGAOPLRLIEKIGGMI 730
614 WDNQNALIKHLLENTFNSSEBAOKTORFYLSCLOVERIEELGAOPLRLIEKIGGMI 673
731 GBEQOLPAVGLTNNHQLFVGFAGVWCVSTPSSHEGLVTDHSPARFVYGLTSLNSRDE 790
674 GBEQOLPAVGLTNNHQLFVGFAGVWCVSTPSSHEGLVTDHSPARFVYGLTSLNSRDE 733
791 LNHFGCPVGSPPMNPQGLCEVW 811
734 LNHFGCPVGSPPMNPQGLCEVW 754
```

RESULT 5

JC521  
 endothelin converting enzyme (EC 3.4.24.-) 1, umbilical vein endothelial cell form - hum  
 C:Species: Homo sapiens (man)  
 C:Date: 17-May-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
 C:Accession: J03521  
 R:Shimada, K.; Matsushita, Y.; Wakabayashi, K.; Takahashi, M.; Matsubara, A.; Iijima, Y.  
 Biochem. Biophys. Res. Commun. 207, 807-812, 1995  
 A>Title: Cloning and functional expression of human endothelin-converting enzyme cDNA.  
 A:Reference number: J03521; MUID:95169128; PMID:7864876  
 A:Accession: J03521  
 A:Molecule type: mRNA  
 A:Residues: 1-758 <SH1>  
 A:Cross-References: GB:043698; NID:g1197803; PIDN:BAA07800.1; PID:g1197804  
 A:Experimental source: umbilical vein endothelial cells  
 C:Genetics:  
 A:Gene: GDB:ECB1; ECB  
 A:Cross-References: GDB:698357; OMIM:600423  
 A:Map position: 1p36.1-p36.1  
 C:Superfamily: neprilysin  
 C:Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; transmembr  
 R:57-77/Domain: transmembrane #status predicted <TM>  
 F:154,175,199,258,304,350,371,527,620,639/Binding site: carboxydrate (Asn) (covalent) #S  
 F:595,599/Binding site: zinc, catalytic (His) #status predicted  
 F:596/Active site: Glu #status predicted

Query Match	59.8%	Score 2561	DB 2	Length 758
Best Local Similarity	60.7%	Pred. No. 2.6e-166		
Matches 477	Conservative 125	Mismatches 150	Indels 34	Gaps 9

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QY 1 PVEGKASPDAMEKVGKASPPSPGP-SPEGMTEGTPRSSSLFMKVTCPHLRSTIGLSRTWV 89
Db 2 PLOG-----JLQNRNPFLOGKRGKRGHOLTSSP-----LPPSLQ-----V 35
QY 90 GFO--KGTROLLGSRTOLEVLVLAGASLLALLLGLCIVALGVQYH-RDPSHSTCITEACI 146
Db 36 NFHSPPSGCGMAARTQVEKRLVVLVLLAGVLVACIALGIQYOTRSP--SVCLSEACV 93
QY 147 RAAGKLLIESIDRGVSPCEDPYQFSCGGMIRNPNPLPDGSRMTFNLSINDONAILKHLLE 206
Db 94 SYTSSILSSNDPVPDPCHPDFSVACGGMKANPVDGSHRMTFNFNLWEHNOAILKHLLE 153
QY 207 NTFNNSSEAEOKTQREYVLSCLQVERIEELGAOPLRDLIEKIGNNITGPMQDNFMEVL 266
Db 154 NST-AVSEAEKRAQVYVYRACMNETRIEELAKPLMEILERIGNNITGPMKADNPDTL 212
QY 267 KAVAGTYRATPPTVVI SADSKSNSNVIQVDSGLPISRDYIINRTANEKYLTAIYDY 326
Db 213 QVTAHYRTSPFSSVYVSADS KNSNSNVIQVDSGLGPSRDYIYNKTENEKVELTGYLNY 272
QY 327 MEELGMLL-GGRPTSTREOMQVLELEQLANITVPOORRBEKTYHMSISELOALAP 385
Db 273 MVOJGLGGGDEAIRAIPOMQJLIDFETALNITIPQEKRDDELIYKVTAAELDTLAP 332
QY 386 SMDWLEFLSLPLSLDSBPVVVYGMDYLAQVSELINRTEPSILNNYILNNLVOKTTS 445
Db 333 AINWLEFLNITIPYVEINSEPIVYVDKEYLEQISTLINTDRCLNNMYIMNLVAKTSS 392
QY 446 SLDRPESAEKLELTYGTRKSCVPRWQTCISNDDALGFLSLFYKATPDRQSKELA 505
Db 393 PLDQRFQADAEKFEVWYGTIKTCLPRWKFCVSDENNLFGLGMPFVYATAEBSKSTA 452
QY 506 EGMISEIRTAFEELAGOLVMMDEKTRQAKAKADAIYMI GPPDEFLIEKELDDVDGYE 565
Db 453 TELILIEKKA FEBSLSTLKMDEBTRKSAKKADAIYMI GPNIMDKELDKYANDYT 512
QY 566 ISEDSFFQNNLANTYNFSAKVMADOLRKPSPSDQMSMTQTVANAYLLPTKNEIVFPAGIIQ 625
Db 513 AVDELTFENAMRPFENFMSWRVTADOLRKAPNEDQMSMTPEMVANAYVSPTEINEIVFPAGIIQ 572
QY 626 APFYANHPKALINNGIGIVNVGHELTHAFDDOGRDYDEKGNLRPMQNESIAAFRHTHC 685
Db 573 APPTYSSPPLALNNGIGIVNVGHELTHAFDDOGRDYDXDGNLRPMKSSVLEAFKQJTC 632

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QY	686	MEQVYQVYNGRLNGRLTGTGENTADNGKAAANNAKALRKGGEQQLPAVGLTNQ	74
Db	633	MVQVYNSVNGEPVNGRRTLTGENTADNGKLAARAQVNWKNQGAHSLPTGLTNQ	692
QY	746	LPEVFGAQVWCVRTPRESSHEGLVTDPHSPARFVLGTLSNSPDLRFHFGCPVQSPMNP	805
Db	693	LPFLFGAQVWCVRTPRESSHEGLVTDPHSPSPFRVIGTSLNSKEPSHFRCPPSPNNP	752
QY	806	QLCEVW	811
Db	753	HKCEVW	758

## RESULT 6

endothelin converting enzyme (EC 3.4.24.-) 1 - bovine  
C:Species: Bos primigenius laurus. (cattle)  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Nov-1999  
C:Accession: A54667; JC2448  
R:Xu, D.; Emoto, N.; Giald, A.; Slaughter, C.; Kaw, S.; dewlt, D.; Yanagiawa, M.  
Cell 78, 473-485, 1994  
A:Title: ECE-1: a membrane-bound metalloprotease that catalyzes the proteolytic activation  
A:Reference number: A54667; MUID:94340737; PMID:8062389  
A:Accession: A54667  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-758 <XUA>  
A:Cross-references: GB:S73774; NID:g897601; PIDN:AAA82928.1; PID:g897602  
R:Ikura, T.; Sawamura, T.; Shiraki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, H.; Shimada,  
Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994  
A:Title: cDNA cloning and expression of bovine endothelin converting enzyme.  
A:Reference number: JC2448; MUID:95032010; PMID:7945289  
A:Accession: JC2448  
A:Molecule type: mRNA  
A:Residues: 1-90, 'A', 92-698, 'A', 700-758 <IKU>  
A:Cross-references: GB:S73774; NID:g688289; PIDN:AA32062.1; PID:g688290  
C:Superfamily: neprilysin  
C:Keywords: hydrolyase; metalloproteinase; transmembrane protein; zinc  
F:57-77/Domain: transmembrane #status predicted <TM>  
F:595,599/Binding site: zinc, catalytic (His) #status predicted  
F:596/Active site: Glu #status predicted

Query Match	59.5%	Score 2546	DB 2	Length 758
Best Local Similarity	59.8%	Pred. No. 2.7e-165		
Matches 474	Conservative 118	Mismatches 160	Indels 40	Gaps 7

[illegible]

OY	440	VOKTSSLDRRFESSQOEKLTLETLYGTKKSCVPRMOTCISINTDDAIGPALGSLFEVATPDR	499
Dd	387	VKRKSSFLDORFOADDEKFMEVMYTKTCLPRMKFCVSIDENTENTGFLGPMFKAYATAE	446
OY	500	QSKEIAEGMISEIRTAPEEALGOVLWMDKTRQAAKERADAIDYMIIGPPDFILBEKELD	559
Dd	447	DSKNIASIILEIKKAPEESLTLKMDEDIRKSAREKADAIYNNIGVPNFIIMDKELD	506
OY	560	VYDGEIEDSDPFOMMLNLNPSACVMAVDOLRKPPSRBQMSMTPTQVNAVYLFTPTNEIVF	619
Dd	507	VFNDTAVPDYJFYENAMRFFNFMSWRVTADOLRKANBRQMSVTPMPVAAVYSPTNIEIVF	566
OY	620	PAGIIQAPFAVRNHFKALNFGIGIGVWMGHETHAFDDGREYDEXGNLRPMNMONESLAAF	679
Dd	567	PAGIIQAPFYTRRSSNALNFGSIGVVGHETHAFDDGREYDXDNGLRPMNKISSVEAF	626
OY	680	RNHRTACMBEOYNQOVNGERLINGROTLGENTIADNGLCRAANYAKWLKIHGBEQOULPAV	739
Dd	627	KQZRLCAWEOJGVNGSVNGEPVNGRITLGENTIALDNGLCRAAYRAYGNWKXGAQEUTLETL	686
OY	740	GLTNHOLFVFVGPAQWCVKRTPBESHGELVYDPHSAPAFVLGITSNSRDCLRHFHCPCVG	799
Dd	687	GLTNQLLFPLFSFGQWCVSVRTPBESHGELITDPHSPRPVIGSISNSKEPSEHHCPBG	746
OY	800	SPANPGOLCEVA 811	
Dd	747	SPANPHKCEVA 758	

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RESULT 7
JC7265
neprilysin (EC 3.4.24.11) II - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: J07265
R:Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A:Title: Neprilysin II: A putative novel metalloproteinase and its isoforms in CNS and testis
A:Reference number: J07265
A:Contents: Brain and testis
A:Accession: J07265
A:Molecule type: mRNA
A:Residues: 1-774 <TAN>
C:Genetics:
A:Gene: nepil
C:Superfamily: neprilysin
C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis; trypsin
Query Match 33.6%; Score 1440; DB 2; Length 774;
Best Local Similarity 38.7%; Pred. No. 6.6e-90;
Matches 295; Conservative 148; Mismatches 261; Indels 58; Gaps 13;

102 RTOLELVAGASLLLAALLGICVALGVQYH-----RDP 135
| | | | | | | | | | | | | | | | | | | | | |
19 RRIAGFECGLIVLTLLMGALIVLVGFYSIGQLPLINSLHVSRRHRTVVKRVLDS 78
| | | | | | | | | | | | | | | | | | | | | |
136 SHST--CLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGMIRRNPLPDGRSRMTFNSTL 193
| | | | | | | | | | | | | | | | | | | | | |
79 SOKSDICTTPSCVIAAARIILQNMDOSSKPCDNFYQACGMVRRHVIPETMSRYSVFDIL 138
| | | | | | | | | | | | | | | | | | | | | |
194 WDQQAQILKHLLENTTFSSSEAEQKQRFVLSCLQVRIEELAQPLRDLIEKIGGNI 253
| | | | | | | | | | | | | | | | | | | | | |
139 RDELVELIKGVLEDSV--QHRPAVEKATKTLFRSCNOSVIEKRSEPLANLDMIGMPV 197
| | | | | | | | | | | | | | | | | | | | | |
254 T-----GP-WDQDNMEVILKAVAGTYRATPTFTVYISADSSKSNSTVQVQDSGLFL 304
| | | | | | | | | | | | | | | | | | | | | |
198 AMDKNETMGPKELERLQAVLNS---QENRRVILDLPIWMDQSSRHVIYIDQPTLGM 254
| | | | | | | | | | | | | | | | | | | | | |
305 PSRYVLLRTANKEKLTAVLYDMELGML-----LGRPFSTREQMQUVELEIQLANI 358
| | | | | | | | | | | | | | | | | | | | | |
255 PSREYFEKEDSH--RVRAYVLOFMTSVATMLRRDLNLPEETDLVOEENAVQLHLETHLANA 313
| | | | | | | | | | | | | | | | | | | | | |

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0Y 359 TVPDQDRDEKIHAKMSISELOAL--APSDHMEFLISFLIS--PLEISDSEPVVVGM 414
Db 314 TVPEKHHDVYALHWRGMBELQERFGLKGNMMLFLIGNVLSSQVVELLPBEEVYVVG 373
0Y 415 YLQGVSELINTEBPSILNNTLYLWLVOKTSSLDLRPESAOBKLETLTYTKSCVPRWQ 474
Db 374 YLEMLBETIDVFPACOTLQNTLYWMLVYLRIGLSLQRPFEKARVDYRKALYGTMMEV--RMR 432
0Y 475 TCISNTDADGAFALGSLFVKATPDRQSKELAEGISLRTAEFEALGOLVMMDEKTRQAA 534
Db 433 ECYSVYVNSNMSAAGSLYIKRAFSDKSKSIYSELIEKTRISFVUNLDELMMDESKKA 492
0Y 535 KEKADAIYDMIGFPDFILBP--KELDDVYDGEYBIEBDSFPQONMLNLYNFSAKVADOLUR 592
Db 493 QEKALNIREQGYDYDYLIEDNNRHLDEBYSLSFSESDLYFENGLONLKNNARQSLUKLRE 552
0Y 593 PPSADQMSMTPTQYNNAYLPTKNEIVPPAGILOAPFAARHNPKALNFGIGIVVMGHELTH 652
Db 553 KVDNMLWITGAAYVAAYFSPNRNLIVPPAGILOPPFSKOQPOLANFGIGIMVIGHELTH 612
0Y 653 APDDQGEYDREGNLRPMQWESLAAFRNHRACBEOYNOYO--VANGERLNGROTIGEN 709
Db 613 GFDNGNRPFDGNGMLDMSNFSARHFRQSQCMITYOYSNFSWELADNONVNGSTIGEN 672
0Y 710 IADNGLKAAYNAVKAMLRKHGEEOQLPAYGLTNHOLFPVGFPAQVWCSVRTPESSHEGLV 769
Db 673 IADNGRQAVKALQWLAEGGRDQRLPGLNLTVAQOLFFIYVAQVWCGSYRPEFAIOSIK 732
0Y 770 TDPSPARFVLTGTLNSRDFLNRHGGCPVSPMNRGOLCEWV 811
Db 733 TDVHSPUKTRYVLSLQNLPGFSEAFHCPRGSVPMHNMNRCTIW 774

```

RESULT 8  
 HYHUN  
 neptilyasin (EC 3.4.24.11) [validated] - human  
 N/Alternate names: C10; common acute lymphocytic leukemia antigen; endopeptidase 24.11  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 08-Dec-2000  
 C/Accession: A41387; A36173; S05275; J10084; S00350; S02228  
 R/D/Adanto, L.; Ship, M.A.; Masteller, E.L.; Reinherz, E.L.  
 A/Title: Organization of the gene encoding common acute lymphoblastic leukemia antigen  
 A/Reference number: A41387; MUID:8936688; PMID:2528730  
 A/Accession: A41387  
 A/Molecule type: DNA  
 A/Residues: 1-750 <DNA>  
 A/Cross-references: GB:M26605  
 A/Note: the authors translated the codon AAC for residues 14 and 72 as Asp  
 R/Ship, M.A.; Richardson, N.E.; Sayre, P.H.; Brown, N.R.; Masteller, E.L.; Clayton, L.H.  
 A/Title: Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA) i  
 A/Reference number: A36173; MUID:88263038; PMID:2968607  
 A/Accession: A36173  
 A/Molecule type: mRNA  
 A/Residues: 1-750 <SH1>  
 A/Cross-references: GB:U03779  
 A/Note: part of this sequence was confirmed by protein sequencing  
 R/Jongeneel, C.V.  
 submitted to the EMBL Data Library, August 1988  
 A/Reference number: S05275  
 A/Accession: S05275  
 A/Molecule type: mRNA  
 A/Residues: 1-750 <JON>  
 A/Cross-references: EMBL:Y00811; NID:G29625; PIDN:CA68752.1; PID:G29626  
 R/Letarte, M.; Vera, S.; Tran, R.; Addie, J.B.L.; Onituka, R.J.; Quackenbush, E.J.; Jong  
 J. Exp. Med. 168, 1247-1253, 1988  
 A/Title: Common acute lymphocytic leukemia antigen is identical to neutral endopeptidase  
 A/Reference number: J10084; MUID:89010526; PMID:2971756  
 A/Accession: J10084  
 A/Molecule type: mRNA  
 A/Status: nucleic acid sequence not shown  
 A/Residues: 2-191;211-737 <LET>

A:Cross-references: EMBL:Y00811  
A>Note: part of this sequence, including the amino end of the mature protein, was confirmed by:  
R.Malfroy, B.; Kuang, W.C.; Seeburg, P.H.; Mason, A.C.; Schofield, P.R.  
FEBS Lett. 229, 206-210, 1988  
A:Title: Molecular cloning and amino acid sequence of human enkephalinase (neutral endopeptidase)  
A:Reference number: S00350; MUID:88152222; PMID:3162217  
A:Accession: S00350  
A:Molecule type: mRNA  
A:Residues: 3-750 <MAL>  
A:Cross-references: EMBL:X07166  
A>Note: 467-Thr was also found  
C:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino side.  
C:Comment: This antigen is an important cell surface marker glycoprotein in the diagnosis of cancer.  
C:Gene: GDB:MMR  
A:Gene: GDB:MMR  
A:Cross-references: GDB:120190; OMIM:120520  
A:Map position: 3q25.1-3q25.2  
A:Insertion: 54/1, 66/1, 120/1, 147/1, 179/1, 218/3, 240/3, 285/3, 319/3, 365/2, 396/3, 431/1, 451/1, 467/1, 471/1, 472/1, 473/1, 474/1, 475/1, 476/1, 477/1, 478/1, 479/1, 480/1, 481/1, 482/1, 483/1, 484/1, 485/1, 486/1, 487/1, 488/1, 489/1, 490/1, 491/1, 492/1, 493/1, 494/1, 495/1, 496/1, 497/1, 498/1, 499/1, 500/1, 501/1, 502/1, 503/1, 504/1, 505/1, 506/1, 507/1, 508/1, 509/1, 510/1, 511/1, 512/1, 513/1, 514/1, 515/1, 516/1, 517/1, 518/1, 519/1, 520/1, 521/1, 522/1, 523/1, 524/1, 525/1, 526/1, 527/1, 528/1, 529/1, 530/1, 531/1, 532/1, 533/1, 534/1, 535/1, 536/1, 537/1, 538/1, 539/1, 540/1, 541/1, 542/1, 543/1, 544/1, 545/1, 546/1, 547/1, 548/1, 549/1, 550/1, 551/1, 552/1, 553/1, 554/1, 555/1, 556/1, 557/1, 558/1, 559/1, 560/1, 561/1, 562/1, 563/1, 564/1, 565/1, 566/1, 567/1, 568/1, 569/1, 570/1, 571/1, 572/1, 573/1, 574/1, 575/1, 576/1, 577/1, 578/1, 579/1, 580/1, 581/1, 582/1, 583/1, 584/1, 585/1, 586/1, 587/1, 588/1, 589/1, 590/1, 591/1, 592/1, 593/1, 594/1, 595/1, 596/1, 597/1, 598/1, 599/1, 600/1, 601/1, 602/1, 603/1, 604/1, 605/1, 606/1, 607/1, 608/1, 609/1, 610/1, 611/1, 612/1, 613/1, 614/1, 615/1, 616/1, 617/1, 618/1, 619/1, 620/1, 621/1, 622/1, 623/1, 624/1, 625/1, 626/1, 627/1, 628/1, 629/1, 630/1, 631/1, 632/1, 633/1, 634/1, 635/1, 636/1, 637/1, 638/1, 639/1, 640/1, 641/1, 642/1, 643/1, 644/1, 645/1, 646/1, 647/1, 648/1, 649/1, 650/1, 651/1, 652/1, 653/1, 654/1, 655/1, 656/1, 657/1, 658/1, 659/1, 660/1, 661/1, 662/1, 663/1, 664/1, 665/1, 666/1, 667/1, 668/1, 669/1, 670/1, 671/1, 672/1, 673/1, 674/1, 675/1, 676/1, 677/1, 678/1, 679/1, 680/1, 681/1, 682/1, 683/1, 684/1, 685/1, 686/1, 687/1, 688/1, 689/1, 690/1, 691/1, 692/1, 693/1, 694/1, 695/1, 696/1, 697/1, 698/1, 699/1, 700/1, 701/1, 702/1, 703/1, 704/1, 705/1, 706/1, 707/1, 708/1, 709/1, 710/1, 711/1, 712/1, 713/1, 714/1, 715/1, 716/1, 717/1, 718/1, 719/1, 720/1, 721/1, 722/1, 723/1, 724/1, 725/1, 726/1, 727/1, 728/1, 729/1, 730/1, 731/1, 732/1, 733/1, 734/1, 735/1, 736/1, 737/1, 738/1, 739/1, 740/1, 741/1, 742/1, 743/1, 744/1, 745/1, 746/1, 747/1, 748/1, 749/1, 750/1, 751/1, 752/1, 753/1, 754/1, 755/1, 756/1, 757/1, 758/1, 759/1, 760/1, 761/1, 762/1, 763/1, 764/1, 765/1, 766/1, 767/1, 768/1, 769/1, 770/1, 771/1, 772/1, 773/1, 774/1, 775/1, 776/1, 777/1, 778/1, 779/1, 780/1, 781/1, 782/1, 783/1, 784/1, 785/1, 786/1, 787/1, 788/1, 789/1, 790/1, 791/1, 792/1, 793/1, 794/1, 795/1, 796/1, 797/1, 798/1, 799/1, 800/1, 801/1, 802/1, 803/1, 804/1, 805/1, 806/1, 807/1, 808/1, 809/1, 810/1, 811/1, 812/1, 813/1, 814/1, 815/1, 816/1, 817/1, 818/1, 819/1, 820/1, 821/1, 822/1, 823/1, 824/1, 825/1, 826/1, 827/1, 828/1, 829/1, 830/1, 831/1, 832/1, 833/1, 834/1, 835/1, 836/1, 837/1, 838/1, 839/1, 840/1, 841/1, 842/1, 843/1, 844/1, 845/1, 846/1, 847/1, 848/1, 849/1, 850/1, 851/1, 852/1, 853/1, 854/1, 855/1, 856/1, 857/1, 858/1, 859/1, 860/1, 861/1, 862/1, 863/1, 864/1, 865/1, 866/1, 867/1, 868/1, 869/1, 870/1, 871/1, 872/1, 873/1, 874/1, 875/1, 876/1, 877/1, 878/1, 879/1, 880/1, 881/1, 882/1, 883/1, 884/1, 885/1, 886/1, 887/1, 888/1, 889/1, 890/1, 891/1, 892/1, 893/1, 894/1, 895/1, 896/1, 897/1, 898/1, 899/1, 900/1, 901/1, 902/1, 903/1, 904/1, 905/1, 906/1, 907/1, 908/1, 909/1, 910/1, 911/1, 912/1, 913/1, 914/1, 915/1, 916/1, 917/1, 918/1, 919/1, 920/1, 921/1, 922/1, 923/1, 924/1, 925/1, 926/1, 927/1, 928/1, 929/1, 930/1, 931/1, 932/1, 933/1, 934/1, 935/1, 936/1, 937/1, 938/1, 939/1, 940/1, 941/1, 942/1, 943/1, 944/1, 945/1, 946/1, 947/1, 948/1, 949/1, 950/1, 951/1, 952/1, 953/1, 954/1, 955/1, 956/1, 957/1, 958/1, 959/1, 960/1, 961/1, 962/1, 963/1, 964/1, 965/1, 966/1, 967/1, 968/1, 969/1, 970/1, 971/1, 972/1, 973/1, 974/1, 975/1, 976/1, 977/1, 978/1, 979/1, 980/1, 981/1, 982/1, 983/1, 984/1, 985/1, 986/1, 987/1, 988/1, 989/1, 990/1, 991

QY HTACIEEDYNDYO---UNGERLNGRQTGENIANGGLKAAYNAVKAMLRKHGEEOQLPA 738  
 682  
 Db OSQCMVYQYNGFMSDMLAGCGHLNGINTLGENIADNGELGQAYRMYQYIKKNGEKLPG 677  
 618  
 QY 739 VGLTNHOLFVGVGAQVWCSTVTPSSHEGLVTDPHSPARRFVIGTLSNSDFLRHCCPV 798  
 739  
 Db 678 IDLNHKKOLFELFNFAQVWCSTVTPREYAVNSIKTVDHSGNFRIGTILQNSAEFSEAFCHRK 737  
 678  
 QY 799 GSPNNPQGLCEVW 811  
 799  
 Db 738 NSYNNPEKKCRKW 750  
 738  
 RESULT 9  
 HYRN  
 N:Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: A29295; A33521  
 R:Malfoy, B.; Schofield, P.R.; Huang, W.J.; Seeburg, P.H.; Mason, A.J.; Henzel, W.J.  
 Biochem. Biophys. Res. Commun. 144, 59-66, 1987  
 A:Title: Molecular cloning and amino acid sequence of rat enkephalinase.  
 A:Reference number: A29295; MUID:87213218; PMID:3555489  
 A:Accession: A29295  
 A:Molecule type: mRNA  
 A:Residues: 1-750 <ML>  
 A:Cross-references: GB:M15944; NID:g204031; PIND:AAA1116.1; PID:g204032  
 A:Note: Part of this sequence, including the amino end of the mature protein, was confir  
 R:Bateman JF., R.C.; Jackson, D.; Slaughter, C.A.; Umhltan, S.; Chai, Y.G.; Moomaw, C.  
 J. Biol. Chem. 264, 6151-6157, 1989  
 A:Title: Identification of the active-site arginine in rat neutral endopeptidase 24.11  
 A:Reference number: A33521; MUID:89197908; PMID:2703483  
 A:Accession: A33521  
 A:Molecule type: Protein  
 A:Residues: 95-102, 'X', 104-129 <BAT>  
 C:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino  
 ney.  
 C:Superfamily: neprilysin  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen  
 F:9-750/Product: neprilysin #status experimental <MAT>  
 F:16-23/Region: scop-transfer sequence  
 F:29-51/Domain: transmembrane #status predicted <TN>  
 F:52-750/Domain: extracellular #status predicted <EXT>  
 F:145-285,325,628/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:311/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:584,588/Binding site: zinc (His) #status predicted  
 F:585/Active site: Glu #status predicted  
 Query Match 29.7%; Score 1272.5; DB 1; Length 750;  
 Best Local Similarity 35.6%; Pred. No. 1.6e-78;  
 Matches 261; Conservative 148; Mismatches 293; Indels 31; Gaps 13;  
 QY 103 TQLELVLAGASLLLAALLIGLVALGVQYHRDPESHSTCTEACRIVAGKILSDRGVSP 162  
 103  
 Db 25 TPLRISLVLALLTLITIAV-TMIALYATY---DDGIKCSDDICKSARILQNNDASAP 79  
 25  
 QY 163 CEDPFPSCGGMIRNPPLPDGRSRMNTFNSLMDNOAILKHLLENTFNSSSEAEQKTOR 222  
 163  
 Db 80 CTDFEKAAGGMLKKNVIFETSSKYSNPDLIRDELIVLKDVOLEPR-TEDIYAVQAKT 138  
 80  
 QY 223 FYLSGLQVERIEELGAOPLRDLIEKIGWNITGF-WDQ--DNFNEVLKAVA--GTYRAT 276  
 223  
 Db 139 LYRSCINSAIDSRGGQGLTLFLPDYIGMPVASQNMWQGTGTSWTAEKSIQLNSKYGK 198  
 139  
 QY 277 PFTYVYISADSKSNSNVITQVDSGLFLPSPDYVLIANTANEKULFAYIDVMEELGMLGG 336  
 277  
 Db 199 VLINEFVGTDDKNSGTQIHFDQRLGLPSRDYECTGTYEACTAVVDPMISVARLRQ 258  
 199  
 QY 337 R---PTSTR---OMQGLLELELIQANITVQDQRPDEEKIYHKMSISELQ-----ALA 384  
 337  
 Db 259 EQRLPIDENQSLSEMKMKMELEKRIANATTPEDBRNDPMILYNNGTILAKQONNSLEING 318  
 259



QY 385 PSMMDMLEPFLSLSP--LEISDSEPVVYGM DYLAQVSELIINRTEPSILNNYLIWNLVOK 442  
 Db 319 KPFMSNFTNEMSTVNINIQNEEVEVVAPEYLTAKRLTKYSPRDIQNLSMRFINMD 378  
 QY 443 TTSSLDREPRESOEKLLETLYGTKSCVPRWOTCISNTD DALGFGLSIFVATPDROSK 502  
 Db 379 LVSSLSRNKESRMKFRKALYGT-TSETATWRCANVYVGNMENAAGRLYVEAAFAFESK 437  
 QY 503 ELAEGNISEIRTAFEALQOLVWMDKTRQAAKEKADALYDMIGPDPFIL-EPEKLDVY 561  
 Db 438 HVEDILIAQIREVFIQTLDLTMMDLETKKAEKALAKERIGYDDDIISNENKLNBY 497  
 QY 562 DGEYISEDSPFQNM LNLNFSAKVMADQLRKPPSRDQMSPTQVAAVYLTPTKNEIVPA 621  
 Db 498 LELANKKEEYFENIIONLKFSSQSKQKLRKYDDEWISGAAYVNAFSSGRNQIVFA 557  
 QY 622 GILQAFYARNHPKALNFGSIGVVMGHELTJHAFDDQREYDKENLPRWQNESLAAPN 681  
 Db 558 GILQPPFPBARQSNISLNYGIGWVIGHEITHGFDNDRFNKDGDLVDWWTQOASANNFQ 617  
 QY 682 HRAQHEQYNOYQ--VNEERLNGRQTLGENTADNGSLKAAAYNAAYKARKHGEQOLPA 738  
 Db 618 GQOCWYQYGNFTWDLAAGQHLNGINTJGENTADNGSIGQAYRAYQNYKNGEELPLPG 677  
 QY 739 VGLTJHQLFFVGFAGVWCVRTPRESSHEGLVTDPHSPARFVLTGTLNSRDLRHPGCV 798  
 Db 678 LDLNKQFLFLNFAQVWCCTYRPEYAVNSIKTDVHSPGNFRITIGLQNSAFEPADAFHCK 737  
 QY 799 GSPMNPQOLCEYV 811  
 Db 738 NSYNMPEKRCRYW 750

## RESULT 10

HYBN  
 neprilysin (EC 3.4.24.11) - rabbit  
 N:Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: A29451; 146872  
 R:Devault, A.; Lazure, C.; Nault, C.; Le Moual, H.; Seldah, N.G.; Chretien, M.; Kahn, P.  
 EMBO J. 6, 1317-1322, 1987  
 A:Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalinase  
 A:Reference number: A29451; MUID:87275825; PMID:2440677  
 A:Accession: A29451  
 A:Molecule type: mRNA  
 A:Residues: 1-751 <DEV>  
 A:Cross-references: EMBL:X05338  
 A:Note: part of this sequence, including the amino end of the mature protein, was confir  
 R:Kahn, P.H.; Powell, J.F.; Beaumont, A.; Roques, B.P.; Mallet, J.J.  
 Biochem. Biophys. Res. Commun. 145, 488-493, 1987  
 A:Title: An antibody purified with a lambda GT11 fusion protein precipitates enkephalin  
 A:Reference number: 146872; MUID:87241544; PMID:3297057  
 A:Accession: 146872  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 207-275 <KAH>  
 A:Cross-references: GB:M16593; NID:G16556; PIDN:AAAS3694.1; PID:G16557  
 C:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino  
 ney.  
 C:Superfamily: neprilysin  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;  
 F:2-751/Product: neprilysin status experimental <MA>  
 F:16-73/Region: stop-transfer sequence  
 F:29-51/Domain: transmembrane #status predicted <TM>  
 F:52-751/Domain: extracellular #status predicted <EX>  
 F:145-286,312,326/Binding site: zinc (His) #status predicted  
 F:585/Binding site: zinc (His) #status predicted  
 F:586/Active site: Glu #status predicted  
 F:629/Binding site: carboxylate (Asn) (covalent) #status experimental  
 Query Match 29.7%; Score 1272; DB 1; Length 751;  
 Best Local Similarity 35.6%; Pred. No. 1.8e-78;

Matches 262; Conservative 150; Mismatches 288; Indels 36; Gaps 13;

QY 103 TQLELVAGASILLAAALIGCLVALGVQYHNDPSHSTCLTACTICRVACKIIESLDRGSP 162  
 Db 25 TPLEISLVLLLVIAV-TWIALYATY---DDGCKSDPCISANLQNMATLEP 79  
 QY 163 CEDFYQSCGQIRRNPLPDGRSMNTFNLSMDQNALIKHLENTFNSSSEAEQTOR 222  
 Db 80 CDFKKAQCGMLKKNVLPETSSRSNFDLRDELVLILKVLQSPK-TEQIVAAQAKT 138  
 QY 223 FYLSCLQYERIEELGAQPLRDLIEKIGMNI-TGEWQD-----DNPEYLKAVAGTY 273  
 Db 139 LYRSCVNETAIDSRGQQLKLPLVYGMPAVATQWEGYGTSGWAEKSIQALNSNYGK 198  
 QY 274 RATPFYTYISADSSSNVYQVDSGLFLPSRQYLRNRANENVLTAYIDYMEELGL 333  
 Db 199 VLINFFV--GTDDKNSNMHIHIDQPLGIPSRDYCTGTGKACCAVYDFMIAVAKL 256  
 QY 334 L---GGRPTSTR---OMQVLELEIOLANITVPQDQRBDEKTYHKNSISELQ----- 381  
 Db 257 IROEGGLPIDENQIVENAKWMELEKATANATKSEDRNDPMLYNKOTLIAQIONNFSLE 316  
 QY 382 ALAPSMDLLEPFLSLPLELS--DSEPVVYVGYMDYLAQVSELIINRTEPSILNNYLIWNL 439  
 Db 317 INKPFMSNFTNEMSTVNINIPNEEDVVAPEYLTAKRLTKYSPRDFQNLFSWR 376  
 QY 440 VQKTTSSLDREPRESOEKLLETLYGTKSCVPRWOTCISNTD DALGFGLSIFVATPD 499  
 Db 377 IMDLVSSLSRYTKOSRNKFRKALYGTTSESA-TWRCANVYVGNMENAAGRLYVEAAAF 435  
 QY 500 QSKELAEGNISEIRTAFEALQOLVWMDKTRQAAKEKADALYDMIGPDPFIL-EPEKLD 558  
 Db 436 ESKHYVEDLIAQIREVFIQTLDLTMMDLETKKAEKALAKERIGYDDDIISNENKLNBY 555  
 QY 559 DVIYDGEYISEDSPFQNM LNLNFSAKVMADQLRKPPSRDQMSPTQVAAVYLTPTKNEIV 618  
 Db 496 NEYLELNKEDYFENIIONLKFSSQSKQKLRKYDDEWISGAAYVNAFSSGRNQIV 555  
 QY 619 PPAQGLQAFYARNHPKALNFGSIGVVMGHELTJHAFDDQREYDKENLPRWQNESLA 678  
 Db 556 PPAQGLQPPFPBARQSNISLNYGIGWVIGHEITHGFDNDRFNKDGDLVDWWTQOASANN 615  
 QY 679 FRNTHACHEQYNOYQ--VNEERLNGRQTLGENTADNGSLKAAAYNAAYKARKHGEQOL 735  
 Db 616 FKESQOCWYQYGNFTWDLAAGQHLNGINTJGENTADNGSIGQAYRAYQNYKNGEELPL 675  
 QY 736 LPAVGLTJHQLFFVGFAGVWCVRTPRESSHEGLVTDPHSPARFVLTGTLNSRDLRHPG 795  
 Db 676 LPQIDLNKQFLFLNFAQVWCCTYRPEYAVNSIKTDVHSPGNFRITIGLQNSAFEPADAF 735  
 QY 796 CPVSGPMNPQOLCEYV 811  
 Db 736 CPKNSYNMPEKRCRYW 751

## RESULT 11

T20003  
 hypothetical protein ZK20.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T20003; T27775  
 R:Gajdasty, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z19209  
 A:Accession: T20003  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-766 <NII>  
 A:Cross-references: EMBL:Z69902; PIDN:CAA3770.1; GSPDB:GN00020; CESP:ZK20.6  
 A:Experimental source: clone C47D12  
 R:Gajdasty, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z20417



## RESULT 13

C88099

protein F18A12.8 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: C88099

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: C88099

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-590 &lt;STO&gt;

A:Cross-references: GB:chr\_11; PIDN:AB66079.1; PID:g2315629; GSPDB:GN00020; CESP:F18A12.

C:Genetics:

A:Gene: F18A12.8

A:Map position: 2

Query Match 26.2%; Score 1122.5; DB 2; Length 590;

Best Local Similarity 38.7%; Pred. No. 1.9e-68;

Matches 229; Conservative 122; Mismatches 220; Indels 21; Gaps 11;

QY 239 QPRLDIKIKGNGNTGP-WDDP--NFMEYLKAVAGTTRATPTPTTYISADSKSSSNVY 295

DB 1 RPLFELTLELGEWPLLOENWMDKTFNFSTLNVSRDYGVDVFFOLYIYADSKNTSRNL 60

QY 296 QVDSQGLPL--PSRDYLYNRANNEKYLTVLYDMEELGML--GGRPTSRBOM----QQ 347

DB 61 FIDOSTLALGRGRDYLLMTTFLSSMTATYRKTLRQIAHLKTDGLTSSSESMADIEK 120

QY 348 VLELEIQLANITVPQDQRDEEKIYHKMSISELQALAPSMWLEFLSPLSELS---- 403

DB 121 IIDFELELAKTIVAEDEERNRNLVYKROIQDLYNLPLQVDWVPFQ-SIAPEDLHLHF 179

QY 404 DSEPVVYVGMQYLOQVSELINRTEPSILNNYLIWNLVQKTTSSLDRFPESQAKLETLY 463

DB 180 NTEIILICEIEYLOHVSSELEIKTDVGLTNYVLMRVQSNVRYLDERFEDIKODFLKVMY 239

QY 464 GTRKSCVPRMOCISTDIALGFLSLFVKATFDSQKEIAEGMISEIRTAEEALGOL 523

DB 240 GQOQS--PRFWKDAQVPSVTLPLAAGATVQAIFQSDGHEALRMIMHLSNSADLVLRQ 298

QY 524 VNMDEKTRQAAEKADAIYDMIGFPDPILEPKELDDVDGYEISE--DSFQNNMLNYS 582

DB 299 DMNDETKVAIEKANSMTINIGYPRVTDLPRLDKQYLGSLSDSDTYIYIMKSVWM 358

QY 583 AKVMADQLKPPSRDQSMTPQTQNAVYLPKNEIYFPAIGILOAPYARHRYALNFGGI 642

DB 359 OSREFQKTRPKHFPDISPAVVNAFYSEPKNAITFPAGIILQPPFSGTFPQAVVYGAI 418

QY 643 GYVMGHELTHAPDQREYDKESGNLRPMQNESLAFRNHTACMEQYNOQYV--NGERL 700

DB 419 GAVLGHETLHGFDDQSQYDKDGNLNMWSESLNSFDRRCITVQYGNVYLPKTNFRY 478

QY 701 NGRQTLGENIADNGGLKAAVNAKAMLRKHGEQQLPAV--GLTNHOLFVGFQAVQVCSY 759

DB 479 NGKLTGEMINADNGGYKEAFQAVQKVTENGSEPRRLPGIQLYTNBGLIFVSYAHFPGCGK 538

QY 760 TPBSSHEGLVTDHPSPARFRVLTGSLNSRDLNHFQCGVSGPMNPGQLCEW 811

DB 539 KEAAMAOQVLTDEHSPFVRVIGVLSNMQAFADVVCPRNAPVNPDKCIW 590

## RESULT 14

T24949

hypothetical protein T16A9.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T24949

R:McMurray, A.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19955

A:Accession: T24949

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-769 &lt;WIL&gt;

A:Cross-references: EMBL:Z77135; PIDN:CA000879.1; GSPDB:GN00023; CESP:T16A9.4

A:Experimental source: clone T16A9

C:Genetics:

A:Gene: CESP:T16A9.4

A:Map position: 5

A:Insertion: 15/2; 59/1; 105/3; 202/1; 336/3; 371/3; 393/1; 424/2; 457/3; 571/1; 637/2; 67

C:Superfamily: nep1lysin

Query Match 23.2%; Score 994.5; DB 2; Length 769;

Best Local Similarity 31.2%; Pred. No. 1.5e-59;

Matches 239; Conservative 153; Mismatches 313; Indels 61; Gaps 19;

QY 96 RQLGSRQLE-LVLAGASILLIAALLGCLVAG----- 129

DB 15 RSCLEKLTLETLVPLGLITALLSVFLMWLDGYKTFDGRPIYPLPFENSSVAV 74

QY 130 ----QYHRDPSHSTLCEACIRVAGKILESDRGVSPCEDFYQFCGGMIRNPLPDGRS 185

DB 75 DRSAKNHD---VCTSRRCVRLAGFLAENLNSKINPCDFFVEFGAGVGNLKNLPANKP 131

QY 186 RNNTNSLMDQNALIKHLENTTNSSEAEOKTQRFYLSCLQVERIEELGAOPLRLDI 245

DB 132 LRHTISDVQSRINKQVKSLSQSPISANEKPMQKAKGYQKCLDEBELESTGEAMRDIA 191

QY 246 EKIGGM-NITG---PWQDNFMEYLKAVAGYRATPTPTTYISADSKSSSNVYQVDS 300

DB 192 KRIIGMPTLEGDQKQWQESHWSWEEQIALVNLGVNAVILIMVAVTDPSSSSSVLELDP 251

QY 301 GLFLPSRDYLYNRANNEKYLTVLYDMEELGMLGGRPTSTRBOMQOQVLEIQLANITV 360

DB 252 KMGAGSRYYLS--GANDPMLRNYTTLMKTVVALGADPAIAKENMEAFPLKLVNPSA 310

QY 361 PODQRDEEKIYHKMSISELQALAPSMWLEFLSPLSPL--ELSDSEPVVYVGMQYLOQV 419

DB 311 DMVRRDRPGRNRRFELMQKSVPPFINPEKLYKTVKELVALSPNHVTIYVEIDYFVGI 370

QY 420 SELINRTEPSILANNYLIWNLVQKTTSSLDRFPESQAKLE---TLYGKSKCVPRMGT 475

DB 371 QHVLQSTPKRYLANIYISRLVQGFSPFLP---PSAREPFOYKANOYGMFNSPPDQWED 427

QY 476 CISTDDALGFLGSLFVKATF--DROSKIEAGMISEIRTAEEALGOLVNMDEKTRQA 533

DB 428 CVTLISVIMDMVGLFVENFPEKERAKKMTL--LTSYIAKNEFIQJLHLDMDDEITRRR 486

QY 534 AKEKADAIYDMIGFPDPILEPKELDDVDGYEISEDSFQNN--LNLNFSAKYVADQL 590

DB 487 AISKANMIYKSGFPVLFNDTWMKMW--GMIIKREYLIHLITIKVLRFTEELL--RL 543

QY 591 RKPSPRDQSMTPQTQNAVYLPKNEIYFPAIGILOAPYARHRYALNFGGI 642

DB 544 DQPLDRSMWFGSPAVDAYTAPNNNEMIFPAGIMOPFLTLGVPNTYTGAVGAVYGHV 603

QY 651 THAFDDQGEYVKEGNLRPMQNESLAAPRNTACMEBOY--NOYVNGE--RLNGRQTLGE 708

DB 604 SHAFDDQGOYBEMGNLDMDALEBEKFIKTRCFVYQYEVNHYVEADIIHLNGQLSLGE 663

QY 709 NIADNGGLKAAVNAKAMLRKHG--EQQLPAV--GLTNHOLFVGFQAVQVCSVTPESSH 765

DB 664 NIADNGGYKTAFNAKAMKSNNTGISBPALPFQGFQFTSQOMFFLAVANNMCSLVAPKHYI 723

QY 766 EGVLTDPHSPARFRVLTGSLNSRDLNHFQCGVSGPMNPGQLCEW 811

DB 724 QILTDVHAPSKYRAMIPLQNNRPEAKAFQCPISGPMNPERKQYW 769

## RESULT 15

HYHUK

Kell blood group protein (EC 3.4.24.-) - human  
N:Alternate names: Kell immunogen

C:Species: Homo sapiens (man)

C&gt;Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #ext\_change 18-Jun-1999

C/Accession: A41127; 152609; 152602

R:Lee, S.; Zambas, E.D.; Marsh, W.L.; Redman, C.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 6353-6357, 1991

A:Title: Molecular cloning and primary structure of Kell blood group protein.

A:Reference number: A41127; PMID:91296819; PMID:1712490

A:Accession: A41127

A:Molecule type: mRNA

A:Residues: 1-732 &lt;LEB&gt;

A:Cross-references: GB:M64934

R:Lee, S.; Mu, X.; Reid, M.; Zelinski, T.; Redman, C.

Blood 85, 912-916, 1995

A:Title: Molecular basis of the Kell (Ki) phenotype.

A:Reference number: 152609; PMID:95152068; PMID:7849312

A:Accession: 152609

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 185-192; 'W', 194-199 &lt;RES&gt;

A:Cross-references: GB:S76770; NID:9914223; PIDN:AAB33389.1; PID:9914224

A&gt;Note: allele KI

R:Lee, S.; Zambas, E.; Green, E.D.; Redman, C.

Blood 85, 1364-1370, 1995

A:Title: Organization of the gene encoding the human Kell blood group protein.

A:Reference number: 152602; PMID:95161764; PMID:7858266

A:Accession: 152602

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 'S', 2-56; 'L', 58-732 &lt;RE2&gt;

A:Cross-references: GB:S76819; NID:9912984; PIDN:AAB33459.1; PID:9912985

C:Comment: This glycoprotein carries the Kell blood group antigens. It is probably a zinc

C:genetics:

A:Gene: GDB:KEL

A:Cross-references: GDB:118742; OMIM:110900

A:Map position: 7q33-7q33

A:Introns: 27/3; 75/1; 134/1; 175/3; 224/3; 245/3; 308/3; 358/2; 401/3; 438/3; 471/3; 49

C:Superfamily: neophilysin

C:Keywords: erythrocyte; glycoprotein; hydrolase; metalloproteinase; surface antigen; tr

F:2-732/Product: Kell blood group protein #status predicted &lt;MAT&gt;

F:48-67/Domain: transmembrane #status predicted &lt;TMN&gt;

F:69-732/Domain: extracellular #status predicted &lt;EXT&gt;

F:94,115,191,345,627,724/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:581,585/Binding site: zinc (His) #status predicted

F:582/Active site: Glu #status predicted

Query Match 22.4%; Score 958.5; DB 1; Length 732;

Best local Similarity 31.3%; Pred. No. 4e-57;

Matches 225; Conservative 130; Mismatches 310; Indels 53; Gaps 13;

QY 114 LLAALLLG---CLVALGVQYHRDPSSHSTLTACTRVAGKILBSLDRGVSPCEDTYQPS 170

DB 48 VLFATLILGLPLCFSVLTFYFQNGCPRPCTSVCLDRHYLAGSNTSVAPCTDFFSFA 107

QY 171 CGGMIRNPLPDGRSRWNTFNSLMDONQILKHLNLTFTNSSSEAEOKTQRFYLSCLQY 230

DB 108 CGPAKKTN-----NSFOELATYKKNLRILILEVONSWHPGSGEKAFOQFYNSCMDT 158

QY 231 ERLEEAGAPLRDLIEIKGSMNITGPMDDNFMELKAVAGTRATPFFTVYISADSKS 290

DB 159 LAIEAGTGLRQVIELGSMRISGKMTSINFRTLRILMSQYGHFPFRAYLGRHPASP 218

QY 291 NSNVIOVDOSGLFLPSRDYILNRTANEK---VLTAYLDYMEELGMILGGRTSTREOQO 346

DB 219 HRFVQIDQ-----PEFDVPLKODQEQIYAQIFREYLFYINQLGTLLGGDPSKVQEHSS 273

QY 347 QVLELEIQLANITVPDQQRDEKIKHKSISSELQALAPMDLEFLSPLSLSDSE 406

DB 274 LSTISITSRFLQPLRPLEQRBAQKLFQWVTIDQLKEMAPADWLSCLOATFTWMSLSFSQ 333

QY 407 PVVYGVMDYLQGVSELINR---TEPSILNNYILNINVOKTSTSLDRRESAQEKLETTY 463  
DB 334 SILVADVLEIKMNSQLVEBMLKQRPFGSHMILGLVLTSLPALSQEQEARRKLSQKLR 393  
QY 464 GTYKS---CVRWOTCISNTDDALGFALGSLFVKATVDRQSKIAEGMISEIRAFEEA 519  
DB 394 ELTEQPPMPARPRRMKCVBEETGTFFEPFLAALFVEAAGPSTRSAMKLPALIRDALYTR 453  
QY 520 LGQLVMDDEKTRQAAKERADALYDMIGPPDFILEBEKLDYVDYGEISBDSFPQMLNLY 579  
DB 454 LNNLPMWMEETNNMAQDKYAQLQVEMGASEMALKFELARQETNDIQLG-SSTLQSVLSCV 512  
QY 580 NFSAYMADQLKPPSRDQWMTPTQVAAAYLPTINEIVFPAGIIOAPFYARNHKALNF 639  
DB 513 RSLRARIQVSFLQPHQRHMKVSPMDVNAVYSVDHVVVFPAGLLQPPFFHGYBRAVNF 572  
QY 640 GGIIVMGHELTAAADDQREYDKGNIRPMTQNSLSLAFRHT-----ACHEBYOYQO 694  
DB 573 GAAGSIMHELTHTF-----YQL---LLP---GGCLACDNLALQEAHLCLKRHYAAR 619  
QY 695 V-NGERLNGROTLGENIADNGGLKAAYNAAYKAMLRKHGEBOQLPAVGLTNHQLPFVGFPAQ 753  
DB 620 LPSRTSPNDSLTFLENADVGGLATLQAYSKRLRHGTYVLSPLDLSPOQIFFRSTAQ 679  
QY 754 VWCSTRTPESSHEGLVTPDHPSPARFVLTGTLNSBDPLRHGCCPVGSPMNPQOLCEW 811  
DB 680 VMCRRPSPQDSH-----DTHSPHLRVHGPISSTAFARVFCARGALLNPSRCQLW 732

Search completed: July 3, 2004, 20:10:04  
Job time : 28 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 19:32:41 ; Search time 18 Seconds  
(without alignments)  
2346.050 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSPPMNGQLCEWV 811

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3820	89.2	787	1 ECE2_HUMAN	O60344 homo sapien
2	3662	85.5	787	1 ECE2_BOVIN	Q10711 bos taurus
3	2592.5	60.6	770	1 ECE1_HUMAN	P42892 homo sapien
4	2567.5	60.0	754	1 ECE1_BOVIN	P42891 bos taurus
5	2556.5	59.7	762	1 ECE1_RAT	P42893 rattus norv
6	2538.5	59.3	754	1 ECE1_CAVPO	P97733 cavia porce
7	1407.5	32.9	775	1 ECE1_RAT	Q9J113 rattus norv
8	1395.5	32.6	775	1 ECE1_MOUSE	Q9J110 mus musculu
9	1389	32.4	775	1 ECE1_HUMAN	O95672 homo sapien
10	1283.5	30.0	749	1 NEP_MOUSE	O61391 mus musculu
11	1282.5	30.0	749	1 NEP_HUMAN	P08473 homo sapien
12	1276.5	29.8	749	1 NEP_RABIT	P08049 oryctolagus
13	1272.5	29.7	749	1 NEP_RAT	P07861 rattus norv
14	1215	28.4	749	1 PEX_HUMAN	P70669 homo sapien
15	1207	28.2	749	1 PEX_MOUSE	P70669 mus musculu
16	994.5	23.2	769	1 YCVL_CAEEL	Q22523 caenorhabd
17	960.5	22.4	732	1 KEIL_HUMAN	P23276 homo sapien
18	583	13.6	647	1 PEPO_LACHE	O52071 lactobacill
19	550	12.8	626	1 PEPO_LACLA	Q07744 lactococcus
20	545	12.7	626	1 YSC6_STRGC	Q09145 lactococcus
21	513	12.0	564	1 YSC6_STRGC	Q09145 streptococ
22	135.5	3.2	1159	1 SOR2_HUMAN	O96827 homo sapien
23	124.5	2.9	4128	1 PRKD_HUMAN	P78527 homo sapien
24	124	2.9	1290	1 SMC4_XENLA	P50532 xenopus lae
25	124	2.9	2376	1 TAO3_YEAST	P40468 saccharomyc
26	123.5	2.9	1181	1 CIAE_BACTL	Q03748 bacillus th
27	121	2.8	2273	1 HPA1_YEAST	P32874 saccharomyc
28	120.5	2.8	680	1 OPDA_SALTY	P27337 salmonella
29	120	2.8	936	1 MSH4_HUMAN	O15457 homo sapien
30	119.5	2.8	1581	1 LMG3_MOUSE	Q97066 mus musculu
31	118	2.8	601	1 CYG5_BUCAI	P57036 buchiera ap
32	116.5	2.7	709	1 HS82_YEAST	P02829 saccharomyc
33	116.5	2.7	1919	1 HAP1_YEAST	P97924 rattus norv

34	115	2.7	514	1 VLI_HPV08	P06417 human papil
35	115	2.7	1060	1 DP3A_LACLA	Q9c170 lactococcus
36	115	2.7	3038	1 TRIO_HUMAN	O75962 homo sapien
37	114.5	2.7	705	1 YNP2_CAEEL	P34562 caenorhabd
38	114.5	2.7	724	1 HMR_HUMAN	O75330 homo sapien
39	114.5	2.7	3829	1 SACS_HUMAN	Q9n2j4 homo sapien
40	114	2.7	836	1 GYRA_MYCGE	P47250 mycoplasma
41	114	2.7	1649	1 YG44_SCHPO	O60179 schizosacch
42	113.5	2.7	662	1 TRB2_RHISN	P55399 rhizobium s
43	113	2.6	680	1 OPDA_ECOLI	P27298 escherichia
44	111.5	2.6	700	1 HS9C_DICDI	P54651 dictyosteli
45	111.5	2.6	1191	1 LMG2_MOUSE	Q61092 mus musculu

## ALIGNMENTS

RESULT 1	ID	ECCE2_HUMAN	STANDARD:	PRT:	787 AA.
AC	O60344	O96NX3	O96NX4		
DT	30-MAY-2000	(Rel. 39, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).				
GN	ECCE2 OR KIA0604.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RP	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS A; B AND C).				
RX	MEDLINE=21575691; PubMed=11718899;				
RA	Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,				
RA	Marsden P.A.;				
RT	"Human endothelin converting enzyme-2 (ECE2): characterization of mRNA				
RT	species and chromosomal localization."				
RL	Biochim. Biophys. Acta 1522:46-52(2001).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM B).				
RC	TISSUE=Brain;				
RC	MEDLINE=98290545; PubMed=9628581;				
RA	Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,				
RA	Nomura N., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. IX.				
RT	The complete sequences of 100 new cDNA clones from brain which can				
RT	code for large proteins in vitro."				
RL	DNA Res. 5:31-39(1998).				
CC	-1- FUNCTION: Converts big endothelin-1 to endothelin-1 (By similarity).				
CC	-1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-				
CC	TRP-Val-22 bond in the precursor.				
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event-Alternative splicing: Named isoforms-3;				
CC	Name=ECE-2A;				
CC	isoId=O60344-1; Sequence=Displayed;				
CC	Name=ECE-2B;				
CC	isoId=O60344-2; Sequence=VSP_005508;				
CC	Name=ECE-2C;				
CC	isoId=O60344-3; Sequence=VSP_005509;				
CC	-1- SIMILARITY: Belongs to peptidase family M13.				
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL; AF428263; AAL30386.1; -				

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DR EMBL: AF428264; AAL30387.1; -.
DR EMBL: AF192531; AAG28399.1; -.
DR EMBL: AB011176; BAA25530.1; -.
DR HSSP: P08473; IDMT.
DR Genem; HGNC:13275; ECE2.
DR MEROPS; M13.003; -.
DR GO: GO:0030659; Cytoplasmic vesicle membrane; IDA.
DR GO: GO:0016511; Fendothelin-converting enzyme activity; IDA.
DR GO: GO:0008270; Zinc ion binding; IDA.
DR GO: GO:0007420; Pibrain development; ISS.
DR GO: GO:0010002; Pibrain development; ISS.
DR GO: GO:0007267; Pibrain development; ISS.
DR GO: GO:0009790; Pibrain development; ISS.
DR GO: GO:0007507; Pibrain development; ISS.
DR GO: GO:0016486; Pibrain development; IDA.
DR GO: GO:0008277; Pibrain development; IDA.
DR GO: GO:0042310; Pibrain development; ISS.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR Pfam; PF01431; Peptidase_M13_N.
DR Pfam; PF05649; Peptidase_M13_N.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE_1.
DR Hydrolase; Metalloprotease; zinc; Glycoprotein; Transmembrane;
KM Signal-anchor; Alternative splicing.
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT METAL 104 787 EXTRACELLULAR (POTENTIAL).
FT ACT SITE 624 624 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 625 625 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 626 628 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 684 684 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 688 688 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 556 556 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 1 63 MOARHAPVQLRWEITMDVRLDPPSPDVLEKGLTDLAL
AGRDPTWTSSEGVHTVDVLS -> MNAVLAQELGAGSN
EYRATLRDEDAPEETPEGGASPDAM (in isoform
ECE-2B).
FT VARSPLIC 1 64 MOARHAPVQLRWEITMDVRLDPPSPDVLEKGLTDLAL
AGRDPTWTSSEGVHTVDVLS -> MNAVLAQELGAGSN
(in isoform ECE-2C).
FT VARSPLIC 1 64 /FTID=VSP_005509.
SEQUENCE 787 AA; 89221 MW; CC2D2B0F0EBF7239 CRC64;
Query Match 89.2%; Score 3820; DB 1; Length 787;
Best Local Similarity 97.8%; Pred. No. 1.5e-248;
Matches 726; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
QY 70 WRVTCPLRLSISGLCSRTWVGFKGTQLGLSRTQLELVLAGSLIAALLGLCVALLGV 129
DB 48 WTVSSSEGVHTVDVLS--VGFKGTQLGLSRTQLELVLAGSLIAALLGLCVALLGV 105
QY 130 QYHRDPSHSTCTLEACIRVAGKILSDRGVSCEDFPYSCCGGIRRRPPLPGRGRWMT 189
DB 106 QYHRDPSHSTCTLEACIRVAGKILSDRGVSCEDFPYSCCGGIRRRPPLPGRGRWMT 165
QY 190 FNSLMPONQAILKHLLENTFSSSEAPKQTFYSCLOVERIEELGAQPLDLLEKIG 249
DB 166 FNSLMPONQAILKHLLENTFSSSEAPKQTFYSCLOVERIEELGAQPLDLLEKIG 225
QY 250 GNAVITGPWDQDNFMEVLKAVAGTYRATPFTVVISADSKSSNSNVIQVDQSGFLPSRDY 309

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DB 226 GNAVITGPWDQDNFMEVLKAVAGTYRATPFTVVISADSKSSNSNVIQVDQSGFLPSRDY 285
QY 310 YNRTANRNVLTAYLDYMEELGMLGCRPTSRBQMOVLLEIOLANITVPQDORRBE 369
DB 286 YNRTANRNVLTAYLDYMEELGMLGCRPTSRBQMOVLLEIOLANITVPQDORRBE 345
QY 370 KLYHMSISELOALAPSMDWLEFLSFLSPELSDSEPVVYGMVLYQVSELRTERPS 429
DB 346 KLYHMSISELOALAPSMDWLEFLSFLSPELSDSEPVVYGMVLYQVSELRTERPS 405
QY 430 IINNTLYNVLVOKTSSLDPRFESAQEKLETLVYTKKSCVPRWOTCISNTDLAGFALG 489
DB 406 IINNTLYNVLVOKTSSLDPRFESAQEKLETLVYTKKSCVPRWOTCISNTDLAGFALG 465
QY 490 SLFVATPDRSKETAEGLSIRTAFFEAALGOLVWMEKROAKERADATYDMIGPPD 549
DB 466 SLFVATPDRSKETAEGLSIRTAFFEAALGOLVWMEKROAKERADATYDMIGPPD 525
QY 550 FLEPKELDVVDGYEISEDSFQOMLNDYNFSAKVMADOLRKPSPDQMSMTPTQVNAV 609
DB 526 FLEPKELDVVDGYEISEDSFQOMLNDYNFSAKVMADOLRKPSPDQMSMTPTQVNAV 585
QY 610 YLPTNKEIVFPAGIIQAPFYANRHPKALNFGSIGVVMGHELTTHARDQGREYDEKGNRP 669
DB 586 YLPTNKEIVFPAGIIQAPFYANRHPKALNFGSIGVVMGHELTTHARDQGREYDEKGNRP 645
QY 670 WMONESIAFRHTACMEQVYQVNGERLNGRGTIGENTADNGLKAAYNAVAKMLRK 729
DB 646 WMONESIAFRHTACMEQVYQVNGERLNGRGTIGENTADNGLKAAYNAVAKMLRK 705
QY 730 HSEBQOLPAVGLTNHQLFVFGPAQVCSVRTPRESSHEGLVTDPHSPARFVLGTLNSRD 789
DB 706 HSEBQOLPAVGLTNHQLFVFGPAQVCSVRTPRESSHEGLVTDPHSPARFVLGTLNSRD 765
QY 790 FLRHFGCPVGSPPMPCQCEW 811
DB 766 FLRHFGCPVGSPPMPCQCEW 787
RESULT 2
EC2_BOVIN STANDARD; PRT; 787 AA.
ID EC2_BOVIN STANDARD; PRT; 787 AA.
AC 010711;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
GN ECE2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OX NCBI_Taxid=9913;
RP SEQUENCE FROM N.A.
RX MEDLINE=95318093; PubMed=7797512;
RA Emoro N., Yanagisawa M.;
RT "Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-
sensitive metalloprotease with acidic pH optimum."
RL J. Biol. Chem. 270:15262-15268 (1995).
CC 1- FUNCTION: Converts big endothelin-1 to endothelin-1. Optimum pH is
5.5. Inactive at neutral pH.
CC 2- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
Tyr-|-val-22 bond in the precursor.
CC 3- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC 4- ENZYME REGULATION: Inhibited by phosphoramidon.
CC 5- SUBUNIT: Homodimer.
CC 6- SUBCELLULAR LOCATION: Type II membrane protein.
CC 7- SIMILARITY: Belongs to peptidase family M13.
CC -----
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CC EMBL; U27341; AAA82927.1; -  
 DR HSP; P08473; IDMT.  
 DR GO; GO:0030651; Cytoplasmic vesicle membrane; ISS.  
 DR GO; GO:001659; P-endothelin-converting enzyme activity; IDA.  
 DR GO; GO:0008270; F-actin binding; ISS.  
 DR GO; GO:0007420; P-brain development; ISS.  
 DR GO; GO:0010002; P-cardioblast differentiation; ISS.  
 DR GO; GO:0007267; P-cell signaling; ISS.  
 DR GO; GO:0009790; P-embryonic development; TAS.  
 DR GO; GO:0007507; P-heart development; ISS.  
 DR GO; GO:001486; P-peptide hormone processing; ISS.  
 DR GO; GO:0008277; P-regulation of G-protein coupled receptor pr. .; TAS.  
 DR GO; GO:0042310; P-vasoconstriction; TAS.  
 DR InterPro; IPR006025; Pept M Zn BS.  
 DR InterPro; IPR00718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 KM Hydrolase; Metalloprotease; zinc; Glycoprotein; Transmembrane; Signal-anchor.  
 KM DOMAIN 1 82  
 FT TRANSMEM 83 103  
 FT DOMAIN 1  
 FT METAL 104 787  
 FT ACT SITE 624 624  
 FT METAL 625 625  
 FT METAL 628 628  
 FT ACT SITE 684 684  
 FT CARBOHYD 688 688  
 FT CARBOHYD 164 164  
 FT CARBOHYD 183 183  
 FT CARBOHYD 187 187  
 FT CARBOHYD 228 228  
 FT CARBOHYD 288 288  
 FT CARBOHYD 333 333  
 FT CARBOHYD 400 400  
 FT CARBOHYD 556 556  
 FT CARBOHYD 649 649  
 FT CARBOHYD 657 657  
 SQ SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CRC64;

Query Match 85.5%; Score 3662; DB 1; Length 787;  
 Best Local Similarity 93.0%; Pred. No. 5.9e-238;

Matches 690; Conservative 22; Mismatches 28; Indels 2; Gaps 1;

QY 70 WVTCPHLRSISGLSRTWVGFQKGRQLGSRTOLELVAGASLLALLLGLCVAGV 129  
 DB 48 WTVSSEGVHTVOVINE--AGFRKRTSRLLGLHTOLELVAGVSLALLLGLCVAGV 105  
 QY 130 QYHRDPSSHTCTEACIRVAGKILSLDRGVSPCEDFYQSGCGWIRNPLPDGSRNWT 189  
 DB 106 QYHRDPSSHTCTEACIRVAGKILSLDRGVSPCEDFYQSGCGWIRNPLPDGSRNWT 165  
 QY 190 FNSLWDONALIKHLENTFNSSSAEOKTORFYVSCIOVRIRIEIGQPLRIIEKIG 249  
 DB 166 FNSLWDONALIKHLENTFNSSSAEOKTORFYVSCIOVRIRIEIGQPLRIIEKIG 225  
 QY 250 GNNITGPMQDQNFMEVLKAVAGYRATPFTVYISADSKSSSNVLOVQSGFLPFSRDY 309  
 DB 226 GNNITGPMQDQNFMEVLKAVAGYRATPFTVYISADSKSSSNVLOVQSGFLPFSRDY 285  
 QY 310 YNRTANEVLTAYLDYMEELGMLGARTSTREMOQVLELEIOLANTITVPQDORRDE 369  
 DB 286 YNRTANEVLTAYLDYMEELGMLGARTSTREMOQVLELEIOLANTITVPQDORRDE 345

QY 370 KIYHMSISELOALAPSDMWLEFLSLPSELSDEPVVVYGYMDYLOQVSELINRTEPS 429  
 DB 346 KIYHMSIAELQALAPSDMWLEFLSLPSELSDEPVVVYGYMDYLOQVSELINRTEPS 405  
 QY 430 ILNNTLNNLVOKTSSLDPRPESAOEKLTLVGTCKKSCYPRWOTCISNTDDALGFLG 489  
 DB 406 ILNNTLNNLVOKTSSLDPRPESAOEKLTLVGTCKKSCYPRWOTCISNTDDALGFLG 465  
 QY 490 SLFVATKDRDSKELAEAGMSEIRPAFEALGOLVWMDKTRQAKERADAIYDMIGPPD 549  
 DB 466 SLFVATKDRDSKELAEAGMSEIRPAFEALGOLVWMDKTRQAKERADAIYDMIGPPD 525  
 QY 550 FILEKELDDVYDGEISEDSFPQWMLNLYNFSAKVMDOLRKPEPSRDQMSWTPQTVAY 609  
 DB 526 FILEKELDDVYDGEISEDSFPQWMLNLYNFSAKVMDOLRKPEPSRDQMSWTPQTVAY 585  
 QY 610 YLPTNKEIVFPAGILQAFYARNHKALNFGIGVWGHETLTHAFDDGREGYDEKGNLRP 669  
 DB 586 YLPTNKEIVFPAGILQAFYARNHKALNFGIGVWGHETLTHAFDDGREGYDEKGNLRP 645  
 QY 670 WMONESLAFRNHTACMEQYNOYVNGERLNGRQTLENTADNGLKAAYNAKMLRK 729  
 DB 646 WMONESLAFRNHTACMEQYNOYVNGERLNGRQTLENTADNGLKAAYNAKMLRK 705  
 QY 730 HGEEOQLPAVGLTNHQLFFVGFAGVWCVRTPRESSHEGLVTDPHSPARFRVLTLSNRD 789  
 DB 706 HGEEOQLPAVGLTNHQLFFVGFAGVWCVRTPRESSHEGLVTDPHSPARFRVLTLSNRD 765  
 QY 790 FLRHFCVGSPPMNGOLCEVW 811  
 DB 766 FLRHFCVGSPPMNGOLCEVW 787

# RESULT 3

ECE1\_HUMAN STANDARD; PRT; 770 AA.  
 ID ECE1\_HUMAN Q9UQ06; Q9UPF4; Q9UPM4; Q9Y501;  
 AC P42892; Q14217; Q9UQ06; Q9UPF4; Q9UPM4; Q9Y501;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).  
 GN ECE1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OK NCBI\_Taxid:9606;  
 RN [1]  
 RP SEQUENCE OF 7-770 FROM N.A. (ISOFORM B).  
 RC TISSUE=Placenta;  
 RX MEDLINE=95104423; PubMed=7805846;  
 RA Schmidt M., Kroeber B., Jacob B., Seubert H., Subkowaki T.,  
 RA Oltner R., Meyer T., Schmalzing G., Hillen H.;  
 RT "Molecular characterization of human and bovine endothelin converting  
 RT enzyme (ECE-1).";  
 RN FEBS Lett. 356:238-243 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RC MEDLINE=95209687; PubMed=7695628;  
 RA Yoritatsu K., Moroi K., Inagaki N., Saito T., Masuda Y.,  
 RA Maesaki T., Seto S., Kimura S.;  
 RT "Cloning and sequencing of a human endothelin converting enzyme in  
 RT renal adenocarcinoma (ACHN) cells producing endothelin-2.";  
 RN Biochem. Biophys. Res. Commun. 208:721-727 (1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM A AND B).  
 RC TISSUE=Placenta;  
 RX MEDLINE=96102029; PubMed=8530372;  
 RA Valdenaire O., Rohrbacher B., Mattei M.-G.;  
 RT "Organization of the gene encoding the human endothelin-converting  
 RT enzyme (ECE-1).";  
 RN J. Biol. Chem. 270:29794-29798 (1995).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).

RA MEDLINE=95169128; PubMed=7864876;  
RA Shimada K., Matsushita Y., Wakabayashi K., Takahashi M., Matsubara A.,  
RA Iijima Y., Tanawa K.;  
RT Cloning and functional expression of human endothelin-converting  
RT enzyme cDNA.";  
RL Biochem. Biophys. Res. Commun. 207:807-812(1995).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC TISSUE=Umbilical vein endothelial cells;  
RA Takayanagi R.;  
RT "Human endothelin-converting enzyme-1c.";  
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 1-132 FROM N.A. (ISOFORM D), AND TISSUE SPECIFICITY.  
RX MEDLINE=99421637; PubMed=10491078;  
RA Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A.,  
RA Vranckx R., Tougaard C., Michel J.-B.,  
RT "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated  
RT from an additional promoter.";  
RL Eur. J. Biochem. 264:341-349(1999).  
RN [8]  
RP SEQUENCE OF 1-103 FROM N.A. (ISOFORM C), FUNCTION, AND TISSUE  
RP SPECIFICITY  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=98060745; PubMed=9396733;  
RA Schweitzer A., Valdenaire O., Neiboeck P., Deuschle U.,  
RA Dumas Mline Edwards J.B., Stumpf J.G., Loeffler B.-M.;  
RT "Human endothelin-converting enzyme (ECE-1): three isoforms with  
RT distinct subcellular localizations.";  
RL Biochem. J. 328:871-877(1997).  
RN [9]  
RP SEQUENCE OF 1-46 FROM N.A. (ISOFORM B).  
RA Baguley C.;  
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 713-770 FROM N.A.  
RA Flowers M.A., Tai S.C., Ballynt C.A., Cheung A.H., Kau C.L.,  
RA Wong G.K.T., Marsden P.A.;  
RT "Characterization of the human endothelin converting enzyme-1 gene  
RT (ECE-1): genomic structure and chromosomal localization.";  
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
RN [1]  
RP FUNCTION: Converts big endothelin-1 to endothelin-1.  
CC [1]- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
CC Trp-[Val-22 bond in the precursor.  
CC [1]- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC [1]- ENZYME REGULATION: Inhibited by phosphoramidon.  
CC [1]- SUBUNIT: Homodimer.  
CC [1]- SUBCELLULAR LOCATION: Type II membrane protein.  
CC [1]- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=B;  
CC IsoId=P42892-1; Sequence=Displayed;  
CC Name=A;  
CC IsoId=P42892-2; Sequence=VSP\_005502;  
CC Name=C;  
CC IsoId=P42892-3; Sequence=VSP\_005504;  
CC Name=D;  
CC IsoId=P42892-4; Sequence=VSP\_005503;  
CC [1]- TISSUE SPECIFICITY: All isoforms are expressed in umbilical vein  
CC endothelial cells, polynuclear neutrophils, fibroblasts, atrium  
CC cardiomyocytes and ventricles. Isoforms A, B and C are also  
CC expressed in placenta, lung, heart, adrenal gland and  
CC phaeochromocytoma; isoforms A and C in liver, testis and small  
CC intestine; isoform B, C and D in endothelial cells and umbilical  
CC vein smooth muscle cells; isoforms C and D in sphenous vein  
CC cells, and isoform C in kidney.  
CC [1]- SIMILARITY: Belongs to peptidase family M13.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL, 235307; CAA84548.1; ALT\_INIT.  
DR EMBL, D49471; BAA08442.1; -.  
DR EMBL, X91922; CAA63015.1; JOINED.  
DR EMBL, X91923; CAA63015.1; JOINED.  
DR EMBL, X91924; CAA63015.1; JOINED.  
DR EMBL, X91925; CAA63015.1; JOINED.  
DR EMBL, X91926; CAA63015.1; JOINED.  
DR EMBL, X91927; CAA63015.1; JOINED.  
DR EMBL, X91928; CAA63015.1; JOINED.  
DR EMBL, X91929; CAA63015.1; JOINED.  
DR EMBL, X91930; CAA63015.1; JOINED.  
DR EMBL, X91931; CAA63015.1; JOINED.  
DR EMBL, X91932; CAA63015.1; JOINED.  
DR EMBL, X91933; CAA63015.1; JOINED.  
DR EMBL, X91934; CAA63015.1; JOINED.  
DR EMBL, X91935; CAA63015.1; JOINED.  
DR EMBL, X91936; CAA63015.1; JOINED.  
DR EMBL, X91937; CAA63015.1; JOINED.  
DR EMBL, X91938; CAA63015.1; JOINED.  
DR EMBL, X91939; CAA63015.1; JOINED.  
DR EMBL, X91923; CAA63016.1; JOINED.  
DR EMBL, X91924; CAA63016.1; JOINED.  
DR EMBL, X91925; CAA63016.1; JOINED.  
DR EMBL, X91926; CAA63016.1; JOINED.  
DR EMBL, X91927; CAA63016.1; JOINED.  
DR EMBL, X91928; CAA63016.1; JOINED.  
DR EMBL, X91929; CAA63016.1; JOINED.  
DR EMBL, X91930; CAA63016.1; JOINED.  
DR EMBL, X91931; CAA63016.1; JOINED.  
DR EMBL, X91932; CAA63016.1; JOINED.  
DR EMBL, X91933; CAA63016.1; JOINED.  
DR EMBL, X91934; CAA63016.1; JOINED.  
DR EMBL, X91935; CAA63016.1; JOINED.  
DR EMBL, X91936; CAA63016.1; JOINED.  
DR EMBL, X91937; CAA63016.1; JOINED.  
DR EMBL, X91938; CAA63016.1; JOINED.  
DR EMBL, X91939; CAA63016.1; JOINED.  
DR EMBL, D43698; BAA07800.1; -.  
DR EMBL, AB031742; BAA83687.1; -.  
DR EMBL, AL0031005; CAA19767.1; -.  
DR EMBL, AJ130828; CAA646443.1; -.  
DR EMBL, X98272; CAA66922.1; -.  
DR EMBL, AL0031728; CAA52285.1; -.  
DR EMBL, AF018034; AAD21221.1; -.  
DR PIR, JC2521; JC2521.  
DR PIR, JC4136; JC4136.  
DR HSP, P08473; IDMT.  
DR MEROPS, M13.002; -.  
DR Genew; HGNC:3146; ECE1.  
DR MIM; 600423; -.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.  
DR InterPro; IPR006025; Pept\_M\_zn\_BS.  
DR InterPro; IPR000718; Peptidase\_M13.  
DR InterPro; IPR008753; Peptidase\_M13\_N.  
DR Pfam; PF01431; Peptidase\_M13; I.  
DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
DR PRINTS; PR00786; NEPRILYSIN.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolyase; Metalloprotease; zinc; Glycoprotein; Transmembrane;  
KW Signal-anchor; Alternative splicing; Polymorphism.  
FT DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT FT (POTENTIAL).  
FT DOMAIN 90 770 EXTRACELLULAR (POTENTIAL).



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FT METAL 607 607 ZINC (CATALYTIC) (BY SIMILARITY)
FT ACT SITE 608 608 BY SIMILARITY.
FT METAL 611 611 ZINC (CATALYTIC) (BY SIMILARITY)
FT METAL 667 667 ZINC (CATALYTIC) (BY SIMILARITY)
FT ACT SITE 671 671 PROTON DONOR (BY SIMILARITY)
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT VARSPLIC 1 44 MAGWPPYVALSALSGMSTYKATLDEEDVDLSLEGDAV

Query Match 60.6%; Score 2592.5; DB 1; Length 770;
Best Local Similarity 59.5%; Pred. No. 3,6e-166;
Matches 484; Conservative 124; Mismatches 152; Indels 53; Gaps 7;

1 MNVALQELGASNMVEYKATLDEPAETPYEGGASPMAMEYKASFPSPGMP 60
9 VALLSALG---MSTYKATLDEEDVDLSLEGDAVPGNLQVNF----- 49
61 GPPRSSGLFMRVTCPLRLSISGLCRITWGFGOKGTQLLGSRTQLELVLAGSLALL 120
50 HSPRSGQR---AATQVKEKLVVLVLLAAGL 80
121 IGLVALGVQYH-RDPSHSTCTEACIRVAGKILSLDRGVSPECEDFYOGSGWIRNP 179
81 VACLAALGIQYOTRSP--SVCLSEACVSYTSLISMDPTVPCDFHFYACGMWIKANP 138
180 LEPGSSRMFTSINDONALIKHLENTTSSSAEOKTQRFYLSCLQVRIEHLAQ 239
139 VPDGHSRMGTFSNLMWHNOAIIKHLENT--ASVSAERKAVYVYRACNMETRIELRAK 197
240 PLRDLIEKGMNITGPMDDNFMELKAVAGYTRATPEFTYISADSSNSNYIQVQ 299
198 PLMELIERGWNITGPMKADNFODLVYTAHRISSPFYSYVADSSNSNYIQVQ 257
300 SGLFPPSRDYLNRTANEKYLTAAYLDYMEELGWL--GGRPTSTREMOQVLELEIOLANI 358
258 SGLGFPNRVYLNKTEKNEKVLGTLYNMQGLKGGGBEALRPQMQLDPTALANI 317
358 TWPOQORDEEKIYHKMSISEIOLAPSDMTLEPLSLPELSDSEPVVYVYGMIDYLOQ 418
318 TIPOEKRRDEELIYHKVTAELQTLAPAINMLPLNTITFYPAEINESBPIVYVDKEYLEQ 377
419 VELINRTPESLINNYLWNLVOKTSSLDRRPESAOEQLLETVIGTKSKSCVPRMOTCS 478
378 ISTLNITDRCLNNMNMNLVKTSSFLDQRPQDDEKFMVWGTGKTKCLPRMFCVS 437
479 NTDDALGFLGSLFVYATFPDROSKEIAEGMISEIRTAPEALGOLVWMDKTRQAKEXA 538
438 DIENNGLGFLGFMFYATFAEDSKSATIILEIKAFESSESTLKMDEEIRKAKEXA 497
539 DAIIYMGEPDITLEKELIDYDGEISEDSFPQNMNLNPSAKVMAOQLRKPPSRQ 598
498 DAIIYMGEPDITLEKELIDYDGEISEDSFPQNMNLNPSAKVMAOQLRKPPSRQ 557
599 WMTDQTVAAVYLLPTKNEIVPAGILQAFYARNHPKALNPGSIGVVMGHELTTHAFDDG 658
558 WMTDQTVAAVYLLPTKNEIVPAGILQAFYARNHPKALNPGSIGVVMGHELTTHAFDDG 617
659 REYDEKGNLRPMWONESLAFRNHTACMEEOYNOYQVNGERLNGRQTLGENTADNGLXA 718
618 REYDEKGNLRPMWONESLAFRNHTACMEEOYNOYQVNGERLNGRQTLGENTADNGLXA 677
719 AYNAYKAMLRKGEBOQLPAVGLTNHQLFFVGPQVQWCVRIPESSHEGLVTDPSPARF 778
678 AYNAYKAMLRKGEBOQLPAVGLTNHQLFFVGPQVQWCVRIPESSHEGLVTDPSPARF 737

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QY 779 RVLGTLNSRDLRFRCGPGVSPMNPQGLCEW 811
DB 738 RVLGTLNSRDLRFRCGPGVSPMNPQGLCEW 770

RESULT 4
BCE1 BOVIN STANDARD; PRT; 754 AA.
AC P42891;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECR-1).
GN BCE1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI TaxID=9913;
RN [1]
RP SEQUENCE FROM N. A., AND PARTIAL SEQUENCE.
RA MEDLINE=95104423; PubMed=7805846;
RA Schmidt M., Kroegeer B., Jacob E., Seubert H., Subkowski T.,
RA Oetler R., Meyer T., Schmalzing G., Hillen H.;
RT "Molecular characterization of human and bovine endothelin converting
RT enzyme (ECE-1).";
RL FEBS Lett. 356:238-243 (1994).
CC -1- FUNCTION: Converts big endothelin-1 to endothelin-1.
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC -1- Val-22 bond in the precursor.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Inhibited by phosphoramidon.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: Belongs to peptidase family M13.
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CC -----
DR EMBL, Z35306; CA884547.1; -
DR FIR, S51010; S47268.
DR HSP, P08473; IDMT.
DR MEROPS, M13.002; -.
DR InterPro, IPR006025; Pept_M_Zn_BS.
DR InterPro, IPR00718; Peptidase_M13.
DR InterPro, IPR008753; Peptidase_M13_N.
DR Pfam, PF01431; Peptidase_M13; 1.
DR Pfam, PF05649; Peptidase_M13_N; 1.
DR PRINTS, PR00786; NEPRILYSIN.
DR PROSITE, PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 53 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT METAL 74 754 EXTRACELLULAR (POTENTIAL).
FT ACT SITE 591 592 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 595 595 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 651 651 PROTON DONOR (BY SIMILARITY).
FT ACT SITE 655 655 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).

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DR		InterPro:	IPR008718;	Peptidase_M13_N.
DR		InterPro:	IPR008753;	Peptidase_M13_N.
DR	Pfam:	PF01431;	Peptidase_M13; 1.	
DR	Pfam:	PF05649;	Peptidase_M13_N; 1.	
DR	PRINTS:	PR00786;	NEPRIIYSIN.	
DR	PROSITE:	PS00142;	ZINC_PROTEASE_1.	
KM		Hydrolase; Metalloprotease; zinc;	Glycoprotein; Transmembrane;	
KW		Signal-anchor; Alternative splicing.		
FT	DOMAIN	1	60	CITOPASMIC (POTENTIAL).
FT	TRANSMEM	61	81	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	82	762	EXTRACELLULAR (POTENTIAL).
FT	METAL	599	599	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	600	600	BY SIMILARITY.
FT	METAL	603	603	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	659	659	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	663	663	PROTON DONOR (BY SIMILARITY).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	308	308	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	354	354	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	375	375	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	531	531	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	643	643	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	VANSPPLIC	1	36	MSLSRPPQGIQLGWSFFLGKKGPGTLVSLPLLASS -> M RLWPEPLRALAALGWSSYKRATLDEEDLVLSISGDVVYN G (in isoform B).
FT	VANSPPLIC	1	36	/FTId=VSP_005505. MSLRPPQGIQLGWSFFLGKKGPGTLVSLPLLASS -> M MSYKRATLDEEDLVLSISGDVVYNG (in isoform C).
FT	VANSPPLIC	1	36	/FTId=VSP_005506. MSLRPPQGIQLGWSFFLGKKGPGTLVSLPLLASS -> M ERLRSVLHALGWSYKRATLDEEDLVLSISGDVVYNG (in isoform D).
FT	VANSPPLIC	1	36	/FTId=VSP_005507. MSLRPPQGIQLGWSFFLGKKGPGTLVSLPLLASS -> M D6B825BC67CCAD8 CRC64;
SEQ	SEQUENCE	762 AA,	86125 MW;	D6B825BC67CCAD8 CRC64;
	Query Match	59.7%;	Score 2556.5;	DB 1; Length 762;
	Best Local Similarity	62.4%;	Pred. No. 9.3e-164;	
	Matches 473;	Conservative 121;	Mismatches 153;	Indels 11; Gaps 6
OY	63	RRSGSLFMR----	VTCHPLR-SIGSLGRITWGQ--	KGTQQLGSRTQLELYLAGSL 114
DB	7	POGLGLQWSSFPFLGKKGPGLTVSLPLLASSLIQVNFSPRSQGRCAWAARSVEKRIVLVLT	66	
OY	115	LIALALLGLVALGYGVHHPDSHTCYCTFACIRAVGKIIESLDRGVSPECDEPYQSCGM	174	
DB	67	LIAAGLVACTAAALGTY-QY-RTRPRPCLTBACSVSISSIIINSNDPIVDPCQDFSTACGM	125	
OY	175	IIRNPLPDGRSKWNTFNNSIMDNQAIIKLKLIENTTFNSSSEAEQKTQREFYLSCLOVERIE	234	
DB	126	IKANVPDPGHSSWGTFNSLMENHOAI IKKLLINST-ASASEAKKAQAYYRYACMMETRIE	184	
OY	235	ELGAPRLADLIEKIGGNVITGPWDONFHEUKAAYGARAFRAFPFTVIYISASKSNSNV	294	
DB	185	EIRAPRLMELLERKLGNNITGPWADNPDTLQVVAHAHRISPFSYVVASDKSNSNV	244	
OY	295	IQVDSGGLFLPSRDYYLNRTANKETYLAVLDVMEELGMLT-CGRPTSTRQOQVLEYLEI	353	
DB	245	IQVDSGGLFLPSRDYYLNRTANKETYLAVLDVMEELGMLT-CGRPTSTRQOQVLEYLEI	304	
OY	354	OLANTIVPQQRDEBEKYHKMSISELOALAPSKMWLEFLSLSPLEISDSEPYYVYGM	413	
DB	305	ALANTITIQEKRRDELHYKHCTAAELQTILAIAIMWLPELAIAIFYPVEINSEBPITYVDK	364	
OY	414	DYLQOVSELINRTESLIANNLYLVOKTTSILDRPESAQEKLETLLYGKSKCVPMW	473	
DB	365	EYLRKVSTLINSTDCKLIANNMYAMLVKRTISSFLQRFDADEKMEVWTGYKTKCLPMW	424	

Oy		47	OTCI SNDDDLAFGLGSLFPKATFGDROSKELASGMSIETAPREALGOLVMMDEKTRA	533
Dd		425	KFCVSDBTENNIGFPLGEMPVAKATPAEDSKAIASEIIILEIKCAFESISLTKMDEDTRRS	484
Oy		534	AKEGADAIYIMIGPPDFILPEPKELDVDYDGYEISEDSFFQNMNLVNFSAKVAMDOLRKP	593
Dd		485	AKERADAIYIMIGPDPNFINDPKELDKVFNDITYAVPDLYFENARPFNPSLRKYTDQLRKA	544
Oy		594	PSRDQSMTPQTUNAYYLPTKNELIVFPAGILLQAFYARNHPKALNFGSIGVMGHELTHA	653
Dd		545	PNRDQMSTPEPMVAAYSPTKNEIVEFPAGILLQAFPYTRSSPDNALNFGSIGVMGHELTHA	604
Oy		654	PDOCGRDYDEGNRPWWOMNESLAEPNNHRACMHEBOYNQVNGERANGROTGEINADN	713
Dd		605	FDDGGRBYDXDGNLRPWKKSSVEAFKQOTECAWQQVNNNSVNGEPAVNGHRTTGENTADN	664
Oy		714	GGLGAANAYNAWKMLRKKGEEQQLPAYVLJTNHOLFVFGFAQWCVSVPRESSHEGLJTDPH	773
Dd		665	GGLGAARAIQNWNKYGKGAQOILFTLGLTNQLFPLGFAQWCVSVRIPRESSHEGLJTDPH	724
Oy		774	SPEARFVLGTLSNSRDFLRHFGCPVGSPMNPGOLCEVW	811
Dd		725	SPSRFVIYGISINSKESEHFRCPLGSPMNPRIHCCEVW	762
RESULT_6				
ID	ECEL_CAVPO	STANDARD;	PRT;	754 AA.
AC	P97739;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
De	Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).			
GN	ECEL1.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.			
OX	NCBITaxID=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96192242; PubMed=8624482;			
RA	Shima H., Yamanouchi M., Omori K., Suglura M., Kawashima K.,			
RA	Sato T.;			
RT	"Endothelin-1 production and endothelin converting enzyme expression			
RL	by guinea pig airway epithelial cells.";			
Biochem. Mol. Biol. Int.	37:1001-1010(1995).			
CC	-1- FUNCTION: Converts big endothelin-1 to endothelin-1.			
CC	-1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-			
CC	trp-[Val-22 bond in the precursor.			
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).			
CC	-1- ENZYME REGULATION: Inhibited by phosphoramidon (By similarity).			
CC	-1- SUBUNIT: Homodimer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-1- SIMILARITY: Belongs to peptidase family M13.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	HSQL; S82653; AAB46734.1; --			
DR	HSPB; P08473; IDMT.			
DR	MEROBS; M13.002; --			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR000718; Peptidase_M13.			
DR	InterPro; IPR008753; Peptidase_M13_N.			
DR	Pfam; PF01431; Peptidase_M13; I.			
DR	Pfam; PF05649; Peptidase_M13_N; 1.			
DR	PRINTS; PR00786; NEPRILYSIN.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1			

KM Hydrolyase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
 KM Signal-anchor.  
 FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 53 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 (POTENTIAL).  
 FT DOMAIN 74 754 EXTRACELLULAR (POTENTIAL).  
 FT METAL 591 591 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 592 592 BY SIMILARITY.  
 FT METAL 595 595 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 651 651 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 655 655 PROTON DONOR (BY SIMILARITY).  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 754 AA; 85772 MW; F064C57FF2BA8A0 CRC64;

Query Match 59.3%; Score 2538.5; DB 1; length 754;  
 Best Local Similarity 58.7%; Pred. No. 1.5e-162;  
 Matches 469; Conservative 128; Mismatches 155; Indels 47; Gaps 5;

QY 14 MVEYKATLDEDAPEFVPGGASPDAMEYKASPPSPSGMTPTGTRSSGLFWRT 73  
 DB 2 MSTRKATLDEBDLVSLSGEYVYVNGLVQV----- 31  
 QY 74 CPHLRISGLCSRTMVGFOKGTROLGSRTOLEVLVLAGSLLAALLGLVALGVYHR 133  
 DB 32 --NFRN-----RSSQRCATRTQVEKGLVVALAAGVACLTALGLQY-R 76  
 QY 134 DPHSTGLTEACIRVAKGILIESLDGVSPCEDFYQSGCGMIRRNPLPDGRSMNTFNSL 193  
 DB 77 TRTPVCLSEACVSVTSIINSNMPTVDCDFPSVCGMIRKAPVDPGSHWGAFSNL 136  
 QY 194 WDNOALIKHLTENTTNSSEAEOKTORYLSTQYERIEELGAQPLRLIKIGWNI 253  
 DB 137 WEHNOALIKHLTENT--ASVSEAEKKAQVYRACWETRIEELRAKLMELIKLQWNI 195  
 QY 254 TGMWDODNFMVEVKAAGVTRATPPFTVYISADSKSSNSNVIOYDQSGFLPSRDYLYNR 313  
 DB 196 TGMWADNFDQTYQVTAHRTSPFESVYVSADSKSNRNVIVHDQSGELPSRDYLYNK 255  
 QY 314 TANEXVLTAYLDYMEELGMLL-GGRPTSTREQWQVLELEIQANITVPODQRDEEIKY 372  
 DB 256 TENEXVLTAYLDYMEELGMLLGGGDEENAIRAQWQIILDFETALANITIPQEKRRDEELTY 315  
 QY 373 HKMSISLOALAPSMQMLEFLSLPLSELDSEPPVYVGMVLYQVSELIINTESLIIN 432  
 DB 316 HKYTAELQVLAIPALINWLPPLNATFYFVEINSEBPVYVKEYLEQVSTLINTTDCCLN 375  
 QY 433 NYLIWLVQKTSLSLRPFESAQEKLETTLYGTKSCVPMQTCISNTDGLFALGSLP 492  
 DB 376 NYWIMLVKRTSSFLDQRFQDADDEKPMHWYGTIKTKLCPMKCVSDTEMLGFGGLGPMF 435  
 QY 493 VKATPFROSKEIAEGMISIRTAEEALGQLVMDEKTRQAKAEKADAYIMIGPFDIL 552  
 DB 436 VKATPFADSKNIASSEILIEIKKAFEEBLSTLKNWDEDETRKSAEKADAYIMIGPFDIM 495  
 QY 553 EPEKLDVYDGYEISESFFQNLNLVNSAKVMAQDLRPPSRDQSMTPQVNAVAYLP 612  
 DB 496 DPEKLDVYDGYEISESFFQNLNLVNSAKVMAQDLRPPSRDQSMTPQVNAVAYLP 555  
 QY 613 TKKEIVFPAGITLAPFARAHPRALNCGGVVMEHLETAAPDOGREYKGNLPPMW 672  
 DB 556 TKKEIVFPAGITLAPFARAHPRALNCGGVVMEHLETAAPDOGREYKGNLPPMW 615  
 QY 673 NESLAAFRNHTACMEQYNOYVNGERLNGRQTLGENIADNGIKKAYNAKMKLRKGE 732

DB 616 NSSVEAFKQOTECMVEQYNSVNGEPPVNGRHITLGENIADNGIKKAYRAYONWVAKNGA 675  
 QY 733 EQLPAAVGLTNQLPFVGAOWCSVTRPSSHEGLYTDPSAPRRVYGTLSNSDFLR 792  
 DB 676 EELPLFLGLTNQLPFVGAOWCSVTRPSSHEGLYTDPSAPRRVYGTLSNSDFLR 735  
 QY 793 HFQCPGSPMNPQLCQEW 811  
 DB 736 HFQCPGSPMNPQLCQEW 754  
 RESULT 7  
 ECEL RAT STANDARD; PRT; 775 AA.  
 ID ECEL RAT 09JHL3: 09J192;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)  
 DE (Damage-induced neuronal endopeptidase).  
 OS RCEL OR XCE OR DINE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Miscar; TISSUE=Brain;  
 RX MEDLINE=20226106; PubMed=10759559;  
 RA Kikyo-Soo S., Sasaki M., Yokohama H., Nakagomi S., Hiyaama T.,  
 RA Aoki S., Wada K., Kiyama H.,  
 RT "Damage-induced neuronal endopeptidase (DINE) is a unique  
 RT metalloproteinase expressed in response to neuronal damage and  
 RT activates superoxide scavengers." Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350 (2000).  
 RL [2]  
 RN SEQUENCE OF 431-632 FROM N.A.  
 RX MEDLINE=99132387; PubMed=9911490;  
 RA Valdenaire O., Richards J.G., Fauli R.L.M., Schweizer A.;  
 RT "XCE, a new member of the endothelin-converting enzyme and neutral  
 RT endopeptidase family, is preferentially expressed in the CNS.";  
 RL Brain Res. Mol. Brain Res. 64:211-221(1999).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides. Cleaves  
 CC the synthetic substrate Z-Gly-Gly-Ileu-pNa and releases pNa. May  
 CC protect against C2-ceramide-induced apoptosis.  
 CC -1- CORFACTOR: Binds 1 zinc ion (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in  
 CC neurons of the caudate putamen, diagonal band, the paraventricular  
 CC nucleus of the thalamus, part of the hypothalamus, in cranial  
 CC motor nuclei, inferior olive, and substantia nigra.  
 CC spinal tract trigeminal nucleus. Not detected in cerebral cortex,  
 CC hippocampus and cerebellum.  
 CC -1- INDUCTION: By mechanical damage to nerve cells.  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL; AB026293; BAA95004.1; -;  
 CC EMBL; AB023896; BAA95006.1; -;  
 CC EMBL; Y16188; CAAT6114.1; -;  
 CC HSSP; P08473; IDMT.  
 CC MEROPS; M13.007; -;  
 CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 CC InterPro; IPR000718; Peptidase\_M13.  
 CC InterPro; IPR008753; Peptidase\_M13\_N.

DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Hydrolyase; Protease; Metalloprotease; Metal-binding; Zinc;  
 KW Glycoprotein; Transmembrane; Signal-anchor.  
 FT DOMAIN 1 61  
 FT TRANSMEM 62 82  
 FT SIGNAL-ANCHOR (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT LUMENAL (POTENTIAL).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 612 775  
 FT ACT SITE 613 613  
 FT METAL 616 616  
 FT METAL 672 672  
 FT METAL 672 672  
 FT CARBOHYD 255 255  
 FT CARBOHYD 322 322  
 FT CARBOHYD 656 656  
 FT CONFLICT 536  
 FT SEQUENCE 775 AA; 87944 MW; 0823091F98A41556 CRC64;

Query Match 32.9%; Score 1407.5; DB 1; Length 775;  
 Best Local Similarity 36.8%; Pred. No. 1,3e-86;  
 Matches 299; Conservative 154; Mismatches 291; Indels 69; Gaps 15;

29 ETPVEGASPDAMEVGKASPFSPGPG--MTPTGTPRSSGLFWVTCPLRLSISG---- 82  
 2 EAPYSTAHAYDERQEVKYSRCTGARGTSLPGRFRRSG-----RSASGARBG 51  
 83 -----LCSRTWGFQKGTQRLGSRTOLEVLVAGASILLALLGLVALGVGYHRD 134  
 52 LPRMNRREVCLLSGVFAAGLCALILAMALAKYLGAGAGTGACGCEG----- 100  
 135 PSHSTCLTACIRVAKILIESLDKGVSPCEDPFQSCGGMIRNPLPDGRSKNTNSLM 194  
 101 PER---FAFAAAFTLSANLDASIDPCQDFYFACGGLRRLHALPDKLTYYGTAAIG 155  
 195 DONQALIKHLENTPTSSSEAEOKTQRFYLSCLQVERIEBELGAOPLDLIEKIGMNT 254  
 156 EQNEERLRRLARPTGPGGAQRKRAFRRSLDMREIERLGRMLLEVIIECGMDIG 215  
 255 GP-----WDQNEEVLKAVAGTYRATPEPTVYISADSKSSNSNVIQVDSGLFLPS 306  
 216 GAADRGGARWDLN---RLLYKAGQVYSAALFSLTIVSLDDRRNSRYIRIDDDGLTPE 272  
 307 RQYLNR--TANRKYTLAYIDYMEELGMLGRTSTREMOQVLEHIOQANTVQ--D 363  
 273 RLYLAQDGESEKVLAAVYVFERLLRLGGA--DAVEQAKOELLQLEORLANISVSEYD 330  
 364 QRDEEKIYHKMSISELQALAPSMWLEFLSPL--ELSDSEPVVYVGYMDYQOVS 420  
 331 LRRDVS SVNKTTLGLOKITRHLQ---KWLDDIQEDDSSEBEVULATDIYQOVS 386  
 421 ELINRTSPILNNYILNVLQKTTSSLDRRPESAOEKLLETLYGTRKSCVPR--WQTCIS 478  
 387 QLRSTPRRIILNHYLVWVYVVLSEHLSPFREALHELAKEMGNDK---PGLAVICG 443  
 479 NTDALGFLGSLFYVATPDROSKELAEAGMISIRAFEBALGQLYMDEKTRQAKEXA 538  
 444 QANRHFGMLGALFVHEHPSAASKAVQOVLVEDIKYILQORLEEDLMDMAQTKAARAL 503  
 539 DAIYDMIGPPDFLEKELDVYDGEISBDSFQWMLNLVNSAKVAMDOLRKPSPRDQ 598  
 504 QYMMWVGVGDFDLKREAVDKYE--PEVIEKTYLKKIILNISIRSIQSLVYKTRQEDVKT 562  
 599 WMTPTQTVNAYYLPTNKEIVPAGILQAFYANRHKALNFGSIGVVMGHELTAFDDG 658  
 563 WLLPQALNAYYLPNGQWVFPAGILQPTLYDDPQISNGYIGIIGIHELTHGYDDWG 622  
 659 REYDKENLRPMWQNSLAFRNHTACMEQYQYOVNERLNGRTLGENTADNGLKA 718  
 623 GQIDRSGNLLHWTEASYSRFLKACCIYLVLYDNFTVYQYVNGKTTLENTADWGLKL 682  
 719 AVNAYKAMLRKHGEQQLPAVGLTNHQLFFVGFAGVWCVRPESHEGLVTDPHSRPF 778

DB 683 AYYAAQKWVREHGPHEPLRLKTYTNHQFFIAPAQWMCIKRSQSYLVLTLDKAPBHY 742  
 QY 779 RVLGTLNSNRDPLRHGCGVSPNPNPGOLCEW 811  
 DB 743 RVLGVSQPEEFGRAFHCPKSPMNVHRCVW 775

## RESULT 8

ECBL MOUSE  
 ID ECBL\_MOUSE STANDARD; PRT; 775 AA.  
 AC Q9JMT0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)  
 GN (Damage-induced neuronal endopeptidase).  
 GN ECBL OR XCE OR DINE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20226106; PubMed=10759559;  
 RA Kikyo-Seo S., Sasaki M., Yokohama H., Nakagomi S., Hirayama T.,  
 RA Aoki S., Wada K., Kiyama H.;  
 RT "Damage-induced neuronal endopeptidase (DINE) is a unique  
 RT metalloproteinase expressed in response to neuronal damage and  
 RT activates superoxide scavengers";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).  
 CC -!- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M13.  
 CC -----  
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 CC -----  
 CC EMBL; AB026294; BAA95005.1; -.  
 DR HSSP; P08473; IDMT.  
 DR MEROPS; M13.007; -.  
 DR MGD; MGI:1343461; Ecbl1.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IDA.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Hydrolyase; Protease; Metalloprotease; Metal-binding; Zinc;  
 KW Glycoprotein; Transmembrane; Signal-anchor.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT SIGNAL-ANCHOR (POTENTIAL).  
 FT TRANSMEM 62 82  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT LUMENAL (POTENTIAL).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 613 613  
 FT METAL 616 616  
 FT METAL 672 672  
 FT METAL 672 672  
 FT CARBOHYD 255 255  
 FT CARBOHYD 322 322  
 FT CARBOHYD 656 656  
 FT SEQUENCE 775 AA; 87993 MW; 53A4595D7C5F34B9 CRC64;

Query Match 32.6%; Score 1395.5; DB 1; Length 775;  
 Best Local Similarity 36.4%; Pred. No. 8.3e-86;  
 Matches 296; Conservative 156; Mismatches 292; Indels 69; Gaps 15;

29 EFTVEGASPDANVEGASPFSPGSPG--MTPGPFRSSGLTMRVYTCPLHSISG----82  
 2 EAVYSMTAHYDEFOEVKTVRCCTGGKRGKSLPPGFRSG-----KASGSRSG 51  
 83 -----LCRTWVGFOKGTROLLGSRTOLELVLAGASILLALLGLCLVALGVYHRD 134  
 52 LPRMNRREVLLGLVFAAGLCALILAMMLKYLGPDAAGGGACPEGC-----100  
 135 PSHSTCTEACTIVAGKILESIDRGVSPCEDFIOFGCGGIMTRNPLPDGSRMNTSLW 194  
 101 PER-----KAFAPAAAPLISANLNASIDPCODFYSAFGGWMRRHAIIPDDLTGTITAAIG 155  
 195 DONOALIKHLENTTFNSSSEADKORFLISCIQVRIEIAQPIRLDIKIGGNIT 254  
 156 EQNEBRRLRLAPPTGGPGGAQKVAFRSCIDMKEIRLGRFMLEVIEDCGGMDLG 215  
 255 GP-----WDODNMEVLKAVAGTYRATPFTVYISADSKSSNVIVQDQGLPLPS 306  
 216 GAADRPAAKWDLN---RLYKQGVYSAALPSLTYSIDRRSSRYVIRIDDGDLTPE 272  
 307 RDTYILNR-TANEXYLINLYDMELGMLGCRPTSTREQOVLLETIOLANTVPO--D 363  
 273 RTIYLAODESEKILAAVRFMORLILIGA--DAVEQKAQELIQLQORLANISVSEYD 330  
 364 QRRDEEKIYHMSISELOALAPSDMELFSLSPF---ELSDPEVYVYGMDDYQOVS 420  
 331 LRNDVSSANKVYLGOLQIKIIPHLOW---KMLIDQIFQEDPSEEEVVLADIDYQVS 386  
 421 ELINRTEPSILNLYLWNLYQKTTSLDRRSPSAOEKILLETLYGTKSCVPR--WOTCIS 478  
 387 QLIRSTPRIRILHYLVKRVVYVSEHLSFPREALHELAKEGNDK---FOELARVCLG 443  
 479 NTDDALGALGSLFYKATPPROSGEIAEGMISEKRTAFEEALGOLVYMDKTOAAXKA 538  
 444 QANRHFEMALGALFVHEHFAASAKYQOLVEDIKYLLQRLBELMDAQOTAKAATAKL 503  
 539 DALYDMIGPFDILPEKLEDDVYDGYEISDSFQONMLNTYNFSACMAALKKRPSRDQ 598  
 504 QYMMWVGDFELKPAVDKEYE-FVHEKTYIKALINSIRSIQLSYKIKIQEYDKST 562  
 599 WSNTPQTVAAYYLPTKNEIYEPAGIIOAPFYARNHPALNFGGIGVYMGHELTAPDDOG 658  
 563 WLPBQALNAYYLIPNKQMYVPAIGIQLPTLYDPPQSLNYYGGITIGHELTGYDDWG 622  
 659 REYDKENLPPWONESLAPRNHTACMEQYNOYQNGERLNGROTLGENIADNGLKA 718  
 623 GQYDRSGNLHMTWTEASRFLHRAECIVRLYDNFTYVYNGRVNGKTLGENDMGGLKL 682  
 719 AYAAYKAMLRKRGEEQOLPAVGLTNHQLPFVGAPOVACSVRTPESSHEGLVDPHSPARF 778  
 683 AYAAYQMVAVKEHPEHHLAKTHNULFPIAPQAMCIRKRSQSYLYOVLTDKHAPEHY 742  
 779 RVIGTISNSRDFLRHFGCVGSPMNPQOLCEW 811  
 743 RVLGSVSGPEEFGRAFHCPKDSPMNPVHKCSVM 775

RESULT 9  
 ECEL\_HUMAN STANDARD; PRT; 775 AA.  
 AC 095672; 09NY95;  
 DT 28-FEB-2003 (Rel. 41, Last Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein).  
 GN ECEL1 OR XCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Caudate, and Spinal cord;  
 RX MEDLINE=99132387; PubMed=991490;  
 RA Valdenaire O., Richards J.G., Paul R.L.M., Schweizer A.;  
 RT "XCE", a new member of the endothelin-converting enzyme and neutral  
 RT endopeptidase family, is preferentially expressed in the CNS.";  
 RL Brain Res. Mol. Brain Res. 64:211-221(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20164043; PubMed=10698686;  
 RA Valdenaire O., Rombracher E., Langeveld A., Schweizer A., Meijers C.;  
 RT "Organization and chromosomal localization of the human ECEL1 (XCE)  
 RT gene encoding a zinc metalloproteinase involved in the nervous control  
 RT of respiration.";  
 RL Biochem. J. 346:611-616(2000).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC -1- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in  
 CC putamen, spinal cord, medulla and subthalamic nucleus. A strong  
 CC signal was also detected in uterine subepithelial cells and around  
 CC renal blood vessels. Detected at lower levels in amygdala,  
 CC caudate, thalamus, pancreas and skeletal muscle. Detected at very  
 CC low levels in substantia nigra, cerebellum, cortex, corpus  
 CC callosum and hippocampus.  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
 CC  
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 CC  
 CC EMBL: Y16187; CAA7613.1; -  
 CC EMBL: AJ130734; CAB86601.1; -  
 CC HSSP: P08473; IDMT.  
 CC MEROPS: M13.007; -  
 CC GeneW: HGNC:3147; ECEL1.  
 DR MIM: 605896; -  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0008237; F: metalloproteinase activity; TAS.  
 DR GO: GO:0007218; P: neuro-peptide signaling pathway; TAS.  
 DR InterPro: IPR006025; Pept\_M\_zn\_BS.  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR008753; Peptidase\_M13\_N.  
 DR Pfam: PF01431; Peptidase\_M13\_1.  
 DR Pfam: PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE\_1.  
 DR HydroLase: Protease; Metalloprotease; Metal-binding; Zinc;  
 KW Glycoprotein; Signal-anchor; Polymorphism.  
 KW CYTOPLASMIC (POTENTIAL).  
 KW SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT TRANSMEM 60 82  
 FT  
 FT DOMAIN 83 775  
 FT METAL 612 612  
 FT ACT\_SITE 613 613  
 FT METAL 616 616  
 FT METAL 672 672  
 FT CARBOHYD 255 255  
 FT CARBOHYD 322 322  
 FT CARBOHYD 656 656  
 FT VARIANT 10 10  
 FT  
 FT VARIANT 328 328  
 FT  
 FT CONFLICT 286 286  
 V -> H (in dbSNP:1529874).  
 /FTID=VAR 012814.  
 V -> I (IN REF. 2).









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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07166; CAA30157.1; ALT_INIT.
DR EMBL; Y00811; CAA68752.1; -.
DR EMBL; J03779; AAA51915.1; -.
DR EMBL; M26628; AAA52294.1; -.
DR EMBL; M26607; AAA52294.1; JOINED.
DR EMBL; M26608; AAA52294.1; JOINED.
DR EMBL; M26609; AAA52294.1; JOINED.
DR EMBL; M26610; AAA52294.1; JOINED.
DR EMBL; M26611; AAA52294.1; JOINED.
DR EMBL; M26612; AAA52294.1; JOINED.
DR EMBL; M26613; AAA52294.1; JOINED.
DR EMBL; M26614; AAA52294.1; JOINED.
DR EMBL; M26615; AAA52294.1; JOINED.
DR EMBL; M26616; AAA52294.1; JOINED.
DR EMBL; M26617; AAA52294.1; JOINED.
DR EMBL; M26618; AAA52294.1; JOINED.
DR EMBL; M26619; AAA52294.1; JOINED.
DR EMBL; M26620; AAA52294.1; JOINED.
DR EMBL; M26621; AAA52294.1; JOINED.
DR EMBL; M26622; AAA52294.1; JOINED.
DR EMBL; M26623; AAA52294.1; JOINED.
DR EMBL; M26624; AAA52294.1; JOINED.
DR EMBL; M26625; AAA52294.1; JOINED.
DR EMBL; M26626; AAA52294.1; JOINED.
DR EMBL; M26627; AAA52294.1; JOINED.
DR PIR; A41387; HYHNH.
DR PDB; 1DMT; 20-DEC-00.
DR PDB; 1DL9; 13-DEC-00.
DR MEROPS; M13.001; -.
DR GeneW; HGNC:7154; NME.
DR MIM; 120520; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0008237; F:metallopeptidase activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Metal-binding; Zinc; Transmembrane;
KW Glycoprotein; Signal-anchor; 3D-structure.
FT INIT_MET 0
FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 28 50 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 51 749 EXTRACELLULAR (POTENTIAL).
FT BINDING 15 22 STOP-TRANSFER SEQUENCE (POTENTIAL).
FT METAL 583 583 SUBSTRATE CARBOXYL (BY SIMILARITY).
FT METAL 587 587 ZINC (CATALYTIC).
FT ACT_SITE 590 590 ZINC (CATALYTIC).
FT METAL 646 646 ZINC (CATALYTIC).
FT ACT_SITE 650 650 PROTON DONOR.
FT DISULFID 56 61
FT DISULFID 79 734
FT DISULFID 87 694
FT DISULFID 142 410
FT DISULFID 233 241
FT DISULFID 620 746
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .).
FT CONFLICT 25 25 P -> R (IN REF. 3).
FT CONFLICT 43 43 T -> R (IN REF. 3).
FT CONFLICT 80 80 T -> R (IN REF. 3).
FT CONFLICT 303 303 T -> R (IN REF. 3).

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	FT	STRAND	55	55
FT	HELI	HELI	59	71
FT	TUR	TUR	74	75
FT	TUR	HELI	78	80
FT	TUR	HELI	82	93
FT	TUR	HELI	98	99
FT	STRAND	HELI	102	104
FT	TUR	HELI	105	121
FT	TUR	HELI	126	127
FT	HELI	HELI	130	143
FT	HELI	HELI	145	150
FT	TUR	HELI	151	153
FT	HELI	HELI	154	159
FT	HELI	HELI	160	163
FT	TUR	HELI	164	164
FT	HELI	HELI	167	169
FT	TUR	HELI	171	172
FT	HELI	HELI	173	176
FT	TUR	HELI	177	180
FT	HELI	HELI	183	194
FT	STRAND	HELI	201	207
FT	TUR	HELI	208	209
FT	STRAND	HELI	210	219
FT	HELI	HELI	228	232
FT	HELI	HELI	235	237
FT	HELI	HELI	238	258
FT	TUR	HELI	259	260
FT	HELI	HELI	265	285
FT	HELI	HELI	289	291
FT	HELI	HELI	295	298
FT	STRAND	HELI	301	303
FT	HELI	HELI	304	310
FT	TUR	HELI	316	317
FT	HELI	HELI	322	330
FT	HELI	HELI	331	333
FT	TUR	HELI	334	334
FT	TUR	HELI	339	340
FT	STRAND	HELI	342	345
FT	HELI	HELI	348	358
FT	TUR	HELI	359	360
FT	HELI	HELI	363	378

Query Match 30.0%; Score 1282.5; DB 1; Length 749;  
 Best Local Similarity 36.0%; Pred. No. 3.1e-78;  
 Matches 264; Conservative 149; Mismatches 289; Indels 31; Gaps 13

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QY 503 ELAEGMISIRTAPEBALGOLVWMDKTRQAAKADAIYDMIPDFIL-EPKELDYY 561
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 437 HVEDLIDIAIRVFIQTLDDLTMDAETKRAEKALIKERIGYDDDIVSNDKLNXY 496
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 562 DGEISEDFQOMLNLNPSAKVMADQKPPSRQMSMTPTQVAAVLYPTKNEIVPFA 621
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 497 LEINVEDYFENIIONLKFSQSKOLREKVDKDEWISGAAVNAFVSSGNQIVPFA 556
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 622 GILQAFVYRNHKLKFGIGVWGMHBLTHAFDDQREYDKENLPPMWNQESLAFFN 681
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 557 GILQPFPSAQSNLSNIGGIGMIVIGHEITHGDDNGKPNKDGDLVDMWTQSNFKE 616
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 682 HTACMEBOYNQYO--VNGERLNGRQTLGEMINADNGLKAAYNAYKMLKGEEOQLPA 738
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 617 QSCQWVYQYGNFSDMLAGGQHLNGINTLGENIADNGLGQAYRAYQNYIKNGEELPLG 676
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 739 VGLTNRQLFPVGAQVWCSTRTPSHSGLVTPDPHAPFVLTGTSNRDPLRHGCEV 798
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 677 LQLNHQLPFLNFAQWCGTYREYVANSIKTDVHSPNFRILIGLQNSAEFSEAFHCRK 736
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 799 GSPMNPOLCEWV 811
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 737 NSYNPEKCKCRW 749
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
NEP RABIT STANDARD; PRT; 749 AA.
ID NEP RABIT
AC 80649;
DT 01-ANG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DE (Enkephalinase) (Neutral endopeptidase 24.11).
GN MME.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=87275825; PubMed=2440677;
RA Devault A., Lazure C., Nault C., le Moual H., Seidah N.G.,
RA Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,
RA Crine P., Boileau G.;
RT "Amino acid sequence of rabbit kidney neutral endopeptidase 24.11
   (enkephalinase) deduced from a complementary DNA.";
RL EMBO J. 6:1317-1322(1987).
RN [2]
RP ERRATUM.
RA Devault A., Lazure C., Nault C., le Moual H., Seidah N.G.,
RA Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,
RA Crine P., Boileau G.;
RL EMBO J. 6:2506-2506(1987).
RN [3]
RP SEQUENCE OF 205-273 FROM N.A.
RX MEDLINE=87241544; PubMed=3297057;
RA Kahn P.H., Powell J.F., Beaumont A., Roques B.P., Mallet J.J.;
RT "An antibody purified with a lambda cIII fusion protein precipitates
   enkephalinase activity.";
RL Biochem. Biophys. Res. Commun. 145:488-493(1987).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=88196403; PubMed=3162886;
RA Devault A., Sales V., Nault C., Beaumont A., Roques B., Crine P.,
RA Boileau G.;
RT "Exploration of the catalytic site of endopeptidase 24.11 by site-
   directed mutagenesis. Histidine residues 583 and 587 are essential
   for catalysis.";
RL FEBS Lett. 231:54-58(1988).
CC -1- FUNCTION: Thermolysin-like specificity, but is almost confined on

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CC acting on polypeptides of up to 30 amino acids. Biologically
CC important in the destruction of opioid peptides such as Met- and
CC leu-enkephalins by cleavage of a Gly-Phe bond.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC hydrophobic residues in insulin, casein, hemoglobin, and a number
CC of other proteins and polypeptides.
CC -1- COFACTOR: Binds 1 zinc ion per subunit.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: Belongs to peptidase family M13.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05338; CAA28950.1; -
DR EMBL; M16593; AAA53694.1; -
DR PIR; A29451; HYRN.
DR HSSP; P08473; IDMT.
DR MEROPS; M13.001; -.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase, Metalloprotease, Metal-binding, Zinc, Transmembrane;
KW Glycoprotein, Signal-anchor.
FT INIT MET 0
FT DOMAIN 1 27 50
FT TRANSMEM 28 50
FT FT
FT FT
FT DOMAIN 51 749
FT DOMAIN 15 22
FT BINDING 102 102
FT METAL 583 583
FT METAL 584 584
FT ACT SITE 587 587
FT METAL 646 646
FT METAL 646 646
FT ACT SITE 650 650
FT DISULFID 56 61
FT DISULFID 79 734
FT DISULFID 87 694
FT DISULFID 142 410
FT DISULFID 233 241
FT DISULFID 620 746
FT CARBOHYD 144 144
FT CARBOHYD 284 284
FT CARBOHYD 310 310
FT CARBOHYD 324 324
FT CARBOHYD 627 627
SQ SEQUENCE 749 AA, 85450 MW, E60B04357B0BAB95 CRC64;

Query Match 29.8%; Score 1276.5; DB 1; Length 749;
Best Local Similarity 35.5%; Pred. No. 7; 7e-78;
Matches 260; Conservative 151; Mismatches 291; Indels 31; Gaps 13;

QY 103 TQLELVLAGASLLLAALLGCLVAGVQYHNPSTCTEACTIVACKILESIDRGVSP 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 24 TPLEISLVLVLLTVIAN-TMIALVATY---DDGICKSDCKISARLLQNM DATYAP 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 CEDFYQSGGWIRRNPLPDGSRWNTPNSLWDQOALIKHLLENTTNSSEAEQKTQR 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 79 CTDFEKYACGWLKXNVIPETSRKSNPDILRDELVLKQVLPK-TEDIVAQQKAKT 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 FYLSCLQYERIBELGAQPLRDLIRKIGWNI-TGSPWQ--DNFMEVLKAVA--GTYRAT 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 IYRSCVNETAIDSRGGQPLKLLPQVGMVPAVQWMEQYGTGWSAEKSIAGLQNSNYGK 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 277 PFFTVYISADSKSSNSNVIQVDQGLFLPSRDYILNRTANEKVLTAVDYMEELGMLT-- 334
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 198 VLINFEVGDGDKNSNNHIIHIDQPLGLPSRDYVETCTGYKACATAYVPMIAVKLITQ 257
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 335 -GGPFTSTRE---QMOQVLELEIQLANITVPDQDRDEEKIYHKMSISELQ-----ALA 384
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 258 BEGLPIDENQISVENMKVMELEKEIATNATTKSEDRNDPMLYNTKMTLAQIQNNFSLIE 317
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 365 PSMDLPELFLSLPLSLS--DSEPVYVGMVYLOQVSLINKRTESILNLTINLVOK 442
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 318 KPFSSNPFNEIMSTVNINIPNEEDVYVAPRYLLKLPKILTKYEPFRDQNLPSWRFIMD 377
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 443 TTSSDRRPESAOEKLLETLYGTCKSCVPMOTCISNTDAGFALGSLFVATPDRQSK 502
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 378 LVSSLSRYTKSRNAPFRKALYGTTSESA-TWRCANVYNGMENNAGRLVDAAPAGEBK 436
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 503 ELAEGMISEIRTAFEALGOLVWMDKTRQAARADALYDMIGPDPFIL-EPKELIDVY 561
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 437 HVEDLLIAQIREVFLOTLDLTMWDAETKKAEKALAIKERIGVDPDDIVSNDKLNNEY 496
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 562 DGEYSEDSSEFQNMALNYPKSAKWADQKRPSPDQMTQVNAVYLPTRKNEIVPFA 621
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 497 LELNKEDEYFENIIQNLKFSQSKQKLEKVDDEWITGAALVAFYSSGRNQLVPPA 556
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 622 GILQAPFYARNHPKALNFGIGVVMGHELTTHAFDDQGREYDKGNLRPMQNESLAAPRN 681
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 557 GILQPPFSAQOQNSLNTYIGMVIHETTHGFDDNGRFNKGDLVDMWTQOASANNPXE 616
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 682 HTACMEBOYNOYO---VNGERLNGRQTLGENTADNGLKAAYNAKWLKRGEEQOLPA 738
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 617 OSQGVVYQGNFSWDLAQGLHNGINTLIGENTADNGIGQAVRAYQNYVKKNGEELKPLG 676
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 739 VGLTHQLPFVFAQVQWCVTRPESSEGLVTDHPSPAFRLVGLTSLNSRDLRHFGCV 798
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 677 IDLNHKQLEFPLFAQVWCGTYRPEYAVNSIKTDVHSPGNFRITIGSLQNSVSESAFOCPK 736
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 799 GSPNMPGOLCEVW 811
   |||||
Db 737 NSYNPEKKCKRW 749
   |||||

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CC CC Important in the destruction of opioid peptides such as Met- and
CC CC Leu-enkephalins by cleavage of a Gly-Phe bond.
CC CC -1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC CC hydrophobic residues in insulin, casein, hemoglobin, and a number
CC CC of other proteins and polypeptides.
CC CC -1- COFACTOR: Binds 1 zinc ion per subunit.
CC CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC CC -1- SIMILARITY: Belongs to peptidase family M13.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL, M15944; AAA41116.1; -.
CC CC DR PIR, A29295; HYRTN.
CC CC DR HSSP, P08473; 1DMT.
CC CC DR MEROPS, M13.001; -.
CC CC DR InterPro, IPR006025; Pept_M_Zn_BS.
CC CC DR InterPro, IPR000718; Peptidase_M13.
CC CC DR InterPro, IPR008753; Peptidase_M13_N.
CC CC DR Pfam, PF01431; Peptidase_M13_1.
CC CC DR Pfam, PF05649; Peptidase_M13_N_1.
CC CC DR PRINTS, PR00786; NEPRILYSIN.
CC CC DR PROSITE, PS00142; ZINC_PROTEASE; 1.
CC CC DR Hydroxylase; Metalloprotease; Metal-binding; Zinc; Transmembrane;
CC CC Glycoprotein; Signal-anchor.
CC CC FT INIT MET 0
CC CC FT DOMAIN 1 27
CC CC FT TRANSMEM 28 50
CC CC FT SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC CC FT DOMAIN 51 749
CC CC FT BINDING 15 22
CC CC FT BINDING 102 102
CC CC FT METAL 583 583
CC CC FT ACT SITE 584 584
CC CC FT METAL 587 587
CC CC FT METAL 646 646
CC CC FT ACT SITE 650 650
CC CC FT DISULFID 56 61
CC CC FT DISULFID 79 734
CC CC FT DISULFID 87 694
CC CC FT DISULFID 142 410
CC CC FT DISULFID 233 241
CC CC FT DISULFID 746
CC CC FT CARBOHYD 144 144
CC CC FT CARBOHYD 210 210
CC CC FT CARBOHYD 284 284
CC CC FT CARBOHYD 310 310
CC CC FT CARBOHYD 324 324
CC CC FT CARBOHYD 627 627
CC CC FT CARBOHYD 627 627
CC CC FT SEQUENCE 749 AA; 85663 MW; 8980ECS0A9016A47 CRC64;
CC CC -----
CC CC Query Match 29.7%; Score 1272.5; DB 1; Length 749;
CC CC Best Local Similarity 35.6%; Pred. No. 1.4e-77;
CC CC Matches 261; Conservative 148; Mismatches 293; Indels 31; Gaps 13;
QY 103 TQLEVLVAGSLTAAALLGLCVNLGVGYHNDPSHSTCTACRIVACKILESLDGRVSP 162
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 24 TPLEISLVVLLTITIV-TWIALYATY---DDGICKSDPCISAKRLIQNMDSAP 78
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 163 CEDFYQSCGGMIRNPLPDRSKRWNTFNSLMDQNALIKHLENTFNSSEADQKQR 222
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 79 CTDPEFYKACGWLKKNVLPETSSRYSNFDLRDELVELITKOVLPQK-TEDIVAVQAKT 137
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 223 FYLSGLQYRIBELGAGPLRLDIKTIQGMNITGP-WDQ-DNFEVLKAVA---GTYPAT 276
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 138 LYRSCINSAISDSRGQPLTLPLDITVGMWPAASQWMEQTYGTSTWAEKSIQNLNSKYKK 197
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 277 PFFTVYISADSKSSNSNVIQVDQGLFLPSRDYILNRTANEKVLTAVDYMEELGMLTGG 336

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Db      198  VLINEFVGTDDKNSVQHITHFDQPRGLPSRDYECTGIYKCACTAYVFMISVARLIRQ 257
      337  R---PTSTR---OMQOVLELEIOLANITVPDORDEEKIYKMSISELQ-----ALA 384
      258  BGRLEPIDEQQLSLENNKWELEKEITANATTKBEDRDPMILYNKMTLATLQNNPSELENG 317
      385  PSMDWLEPLSLSP--LELSDEPVYVGMIDLOQVSELINRTEPSLIINNTYLINLVOK 442
      318  KPFSSNFTNEIMSTVINIIONEBEVYVAPBYLTCLKPILTKYSPRDQLNLSMRPIND 377
      443  TTSSLDREPSAOEKLLETLYGTKKSCVPRMOTCISNTDLAGPALGSLFVKATPDRSG 502
      378  LVSSLSRNTKESNNAFRKALYGI-TSEIATWRKANYVGNENNAVGRLYVEAPAGSEK 436
      503  EIAEGMISIRTAFEELGOLVWDEKTRQAAKEKADAYDIGPPDIL-EPKELDDVY 561
      437  HVVEDLIAQIREVFIOTLDDLTMMDAFETKKAEKALAIKERIGYDDIISNENKLNXY 496
      562  DGEIISEDSPFQNMILNYPKAWADQLRKPPSRDQMSMTQTVNAYTLPTKNEIVPPA 621
      497  LEIANYEEEFENIIIONLKFSSQSKOLKREKVDKDEWISGAVNAFVSSGRNQIVPFA 556
      622  GILQAPFYARNHPKALNPGIGVVMGHELTTHAFDDQGREYDKGNLRPMWQNESLAAPRN 681
      557  GILQPPFARQSNLSINLYGIGVIGHEITHGFDGGRFNKDGDLVDMWTOOSANNFQD 616
      682  HTACMEEQNOYO--VNGERLNGRQTLGENTADNGLKAANYAVKMLRKGEEOQLPA 738
      617  QSGCWVYQGNFTWDLAAGGHLNGITLLENTADNGIGIQARAYGNVYKKGEBELTFC 676
      739  VGLTHQLFFVGAQVQVCRTPRESSHEGLVDPHSPAPFRVLGTSNRDPLRHFGCV 798
      677  LDLNHQLPFLNFAQVCGTYRBEVAVNSIKTDVHSPGNFRITGLQNSAEFADAFHCCK 736
      799  GSPNPNQGLCEVY 811
      737  NSYNPDKRCRWY 749
      737  NSYNPDKRCRWY 749

QY      799  GSPNPNQGLCEVY 811
      737  NSYNPDKRCRWY 749

Db      737  NSYNPDKRCRWY 749

RESULT 14
PEX_HUMAN
ID_PEX_HUMAN STANDARD: PRT: 749 AA.
AC P78562; 000678; Q13646; Q93032; Q99827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphate regulating neutral endopeptidase (EC 3.4.24.-)
DE (Metalloendopeptidase homolog PEX (X-linked hypophosphatemia protein)
DE (HYP) (Vitamin D-resistant hypophosphatemic rickets protein).
OS Homo sapiens (Human).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS HYP ARG-85; LEU-534; ARG-579 AND
RP PRO-651.
RX MEDLINE=97343325; PubMed=9199930;
RA Brandau F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,
RA Brancas O., Mohnik K.L., Cagnoli M., Steffens C., Klages S.,
RA Borzym K., Pohl T., Oudet C.L., Econs M.J., Rowe P.S.N., Reinhardt R.,
RA Weitingner T., Lehrach H.;
RT "Genomic organization of the human PEX gene mutated in X-linked
RT dominant hypophosphatemic rickets.";
RL genome Res. 7:573-585(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97332252; PubMed=9077527;
RA Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,
RA Goodyer C.G., Tenenhouse H.S.;
RT "PeX/PEX tissue distribution and evidence for a deletion in the 3'
RT region of the Pex gene in X-linked hypophosphatemic mice.";
```

```

RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone;
RX MEDLINE=97343443; PubMed=9199999;
RA Guo R., Quarles L.D.;
RT "Cloning and sequencing of human PEX from a bone cDNA library:
RT evidence for its developmental stage-specific regulation in
RT osteoblasts.";
RL J. Bone Miner. Res. 12:1009-1017(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Lipman M.L., Panda D., Henderson J.E., Shen Y., Goltzman D.,
RA Karpelis A.C.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224400; PubMed=9070661;
RA Grieff M., Mumm S., Maeltz P., Mazzarella R., Whyte M.P.,
RA Thakker R.V., Schlessinger D.;
RT "Expression and cloning of the human X-linked hypophosphatemia gene
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 231:635-639(1997).
RN [6]
RP SEQUENCE OF 4-641 FROM N.A.
RX MEDLINE=96024647; PubMed=7550339;
RA Francis F., Hennig S., Korn B., Reinhardt R., de Jong P., Pousetka A.,
RA Lehrach H., Rowe P.S.N., Goulding J.N., Sumnerfield T., Mountford R.,
RA Read A.P., Popowska E., Pronicka E., Davies K.B., Orlordan J.L.H.,
RA Econs M.J., Nesbitt T., Dreznar M.K., Oudet C.L., Pannetier S.,
RA Hanauer A., Strom T.M., Meindl A., Lorenz B., Cagnoli M.,
RA Mohnik K.L., Murken J., Weitingner T.;
RT "A gene (PEX) with homologies to endopeptidases is mutated in
RT patients with X-linked hypophosphatemic rickets. The HYP
RT Consortium.";
RL Nat. Genet. 11:130-136(1995).
RN [7]
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.;
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP VARIANTS HYP TYR-85; CYS-166; SER-252; ILE-253 AND VAL-579.
RX MEDLINE=97260404; PubMed=9106524;
RA Holm I.A., Huang X., Kunkel L.M.;
RT "Mutational analysis of the PEX gene in patients with X-linked
RT hypophosphatemic rickets.";
RL Am. J. Hum. Genet. 60:790-797(1997).
RN [9]
RP VARIANTS HYP SER-77; PRO-138; LEU-534 AND ARG-579.
RX MEDLINE=9725287; PubMed=9097956;
RA Rowe P.S.N., Oudet C.L., Francis F., Sindling C., Pannetier S.,
RA Econs M.J., Strom T.M., Weitingner T., Garabedian M., David A.,
RA Macher M.-A., Questiaux E., Popowska E., Pronicka E., Read A.P.,
RA Mokrzycki A., Glorieux F.H., Dreznar M.K., Hanauer A., Lehrach H.,
RA Goulding J.N., Orlordan J.L.H.;
RT "Distribution of mutations in the PEX gene in families with X-linked
RT hypophosphatemic rickets (HYP).";
RL Hum. Mol. Genet. 6:539-549(1997).
RN [10]
RP VARIANT HYP PRO-555.
RX MEDLINE=98439582; PubMed=9768646;
RA Econs M.J., Friedman N.B., Rowe P.S.N., Speer M.C., Francis F.,
RA Strom T.M., Oudet C.L., Smith J.A., Nimmiya J.T., Lee B.B.,
RA Bergen H.;
RT "A PEX gene mutation is responsible for adult-onset vitamin
RT D-resistant hypophosphatemic osteomalacia: evidence that the disorder
RT is not a distinct entity from X-linked hypophosphatemic rickets.";
RL J. Clin. Endocrinol. Metab. 83:3459-3462(1998).
RN [11]
RP VARIANTS HYP PHE-317; LEU-534; ARG-579; ARG-621; ASN-680 DEL; THR-720;
RP TYR-731 AND ARG-749.
RX MEDLINE=98439610; PubMed=9768674;
RA Dixon P.H., Christie P.T., Wooding C., Trump D., Grieff M., Holm I.A.,
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RA Gertner J.M., Schmidtke J., Shah B., Shaw N., Smith C., Tau C.,  
 RA Schlesinger D., Whyte M.P., Thakker R.V.;  
 RT "Mutational analysis of PHEX gene in X-linked hypophosphatemia.",  
 RL J. Clin. Endocrinol. Metab. 83:3615-3623(1998).  
 [12]  
 RP VARIANTS HYP SER-80; PHE-142; GLY-237; CYS-530; ASP-573; SER-733 AND  
 RP TRP-746.  
 RX MEDLINE=99368844; PubMed=10439971;  
 RA Filisetti D., Ostermann G., von Bredow M., Strom T.M., Filler G.,  
 RA Ethlich J., Panietier S., Garnier J.-M., Rowe P.S.N., Francis F.,  
 RA Juliette A., Hanauer A., Econs M.J., Oudet C.L.;  
 RT "Non-random distribution of mutations in the PHEX gene, and  
 RT under-detected missense mutations at non-conserved residues.",  
 RL Eur. J. Hum. Genet. 7:615-619(1999).  
 [13]  
 RP VARIANTS HYP PHE-85; PRO-141; VAL-341 DEL; PRO-567; LYS-680 AND  
 RP TYR-693.  
 RX MEDLINE=20202840; PubMed=10737991;  
 RA Tyynismaa H., Kaitila I., Naentoe-Salonen K., Ala-Houhala M.,  
 RA Alitalo T.;  
 RT "Identification of fifteen novel PHEX gene mutations in Finnish  
 RT patients with hypophosphatemic rickets.",  
 RL Hum. Mutat. 15:383-384(2000).  
 [14]  
 RP VARIANTS HYP ARG-160 AND ASN-444 INS.  
 RX MEDLINE=20461419; PubMed=11004247;  
 RA Sato K., Tajima T., Nakae J., Adachi M., Asakura Y., Tachibana K.,  
 RA Suga S., Katsumata N., Tanaka T., Hayashi Y., Abe S., Mutsaers M.,  
 RA Okhara K., Shinohara N., Fujieda K.;  
 RT "Three novel PHEX gene mutations in Japanese patients with X-linked  
 RT hypophosphatemic rickets.",  
 RL Pediatr. Res. 48:536-540(2000).  
 CC -1- FUNCTION: Probably involved in bone and dentin mineralization  
 CC and renal phosphate reabsorption.  
 CC -1- COPACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Lymphocyte and fetal brain; not in adult  
 CC brain, placenta, skeletal muscle and pancreas; not in adult and  
 CC fetal heart, lung, liver and kidney.  
 CC -1- DISEASE: Defects in PHEX are a cause of X-linked hypophosphatemic  
 CC rickets (HYP) [MIM:307800]. HYP is an X-linked dominant disorder  
 CC characterized by impaired phosphate uptake in the kidney, which is  
 CC likely to be caused by abnormal regulation of sodium phosphate  
 CC cotransport in the proximal tubules. Clinical manifestations  
 CC include skeletal deformities, growth failure, craniosynostosis,  
 CC extrarenal calcifications, pseudofractures in lower  
 CC extremities, and muscular hypotonia with onset in early childhood.  
 CC X-linked hypophosphatemic rickets is the most common form of  
 CC hypophosphatemia with an incidence of 1 in 20000.  
 CC -1- SIMILARITY: Belongs to phosphatase family M13.  
 CC -1- DATABASE: NAME=PHEXdb; WWW="http://data.mcgill.ca/phexdb/".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
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 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating neutral endopeptidase) (X-linked hypophosphatemia protein) (HYP) (Vitamin D-resistant hypophosphatemic rickets protein).  
 GN PHEX OR PEX OR HYP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 RX MEDLINE=96411643; PubMed=8812412;  
 RA Du L., Desbarats M., Viel J., Glorieux P.H., Cawthorn C., Escarot B.;  
 RT "cDNA cloning of the murine Pex gene implicated in X-linked hypophosphatemia and evidence for expression in bone.";  
 RL Genomics 36:22-28(1996).  
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 RX MEDLINE=97217775; PubMed=9063736;  
 RA Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,  
 RA Lehnach H., Meitinger T.;  
 RT "Pex gene deletions in Cy and Hyp mice provide mouse models for X-linked hypophosphatemia.";  
 RL Hum. Mol. Genet. 6:165-171(1997).  
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 RC STRAIN=C57BL/6J;  
 RX MEDLINE=9723252; PubMed=9077527;  
 RA Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,  
 RA Goodyer C.G., Tenenhouse H.S.;  
 RT "Pex/pex tissue distribution and evidence for a deletion in the 3' region of the Pex gene in X-linked hypophosphatemic mice.";  
 RL J. Clin. Invest. 99:1200-1209(1997).  
 CC -1- FUNCTION: Probably involved in bone and dentin mineralization and renal phosphate reabsorption.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Bone.  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).  
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 DR EMBL; U74223; AAC26275.1; -  
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 DR EMBL; U74229; AAC26281.1; -  
 DR EMBL; U74230; AAC26282.1; -  
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 DR EMBL; U74232; AAC26284.1; -  
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 DR EMBL; U74313; AAC26365.1; -  
 DR EMBL; U74314; AAC26366.1; -  
 DR EMBL; U74315; AAC26367.1; -  
 DR EMBL; U74316; AAC26368.1; -  
 DR EMBL; U74317; AAC26369.1; -  
 DR EMBL; U74318; AAC26370.1; -  
 DR EMBL; U74319; AAC26371.1; -  
 DR EMBL; U74320; AAC26372.1; -  
 DR EMBL; U74321; AAC26373.1; -  
 DR EMBL; U74322; AAC26374.1; -



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 16:38:11 ; Search time 70 Seconds

(without alignments)  
3655.504 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSFPMNPQLCEVW 811

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeopl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4281	100.0	811	4 Q8NFD7	Q8NFD7 homo sapien
2	3820	89.2	765	6 Q8E5C2	Q8E5C2 bos taurus
3	3772	88.1	816	6 Q8E5C2	Q8E5C2 bos taurus
4	3695	86.3	763	11 Q923T6	Q923T6 mus musculus
5	3665	85.6	763	11 Q80Z57	Q80Z57 mus musculus
6	3659.5	85.5	736	6 Q8E5C3	Q8E5C3 bos taurus
7	3624	84.7	814	11 Q80Z59	Q80Z59 mus musculus
8	3572.5	83.5	785	11 Q80Z60	Q80Z60 mus musculus
9	3556	83.1	734	11 Q80Z58	Q80Z58 mus musculus
10	3371	78.7	709	11 Q8C099	Q8C099 mus musculus
11	2653	62.0	752	13 Q9DGM6	Q9DGM6 gallus galli
12	2574	60.1	752	13 Q7ZTR3	Q7ZTR3 xenopus lae
13	2554	59.7	758	6 Q28868	Q28868 bos taurus
14	2546	59.5	758	6 Q28010	Q28010 bos taurus
15	2352.5	55.0	526	11 Q8K0P0	Q8K0P0 mus musculus
16	1810	42.3	727	5 Q81S64	Q81S64 locusta mtg

17	1647	38.5	786	5 Q9W5Y0	Q9W5Y0 drosophila
18	1647	38.5	786	5 Q8W5S1	Q8W5S1 drosophila
19	1521	35.5	849	5 Q9W436	Q9W436 drosophila
20	1452	33.9	770	4 Q96PH9	Q96PH9 homo sapien
21	1442.5	33.7	742	11 Q9ERK3	Q9ERK3 mus musculus
22	1431	33.4	765	11 Q9JL13	Q9JL13 mus musculus
23	1430.5	33.4	742	11 Q9QZV6	Q9QZV6 mus musculus
24	1427	33.3	779	11 Q9BRK2	Q9BRK2 mus musculus
25	1419	33.1	765	11 Q9QZV7	Q9QZV7 mus musculus
26	1398.5	32.7	845	4 Q8ETM4	Q8ETM4 homo sapien
27	1373.5	32.1	976	5 Q91714	Q91714 drosophila
28	1373.5	32.1	1040	5 Q8T062	Q8T062 drosophila
29	1321	30.9	770	5 Q9UPF2	Q9UPF2 hydra attenu
30	1290.5	30.1	750	11 Q8K251	Q8K251 mus musculus
31	1290	30.1	848	5 Q16796	Q16796 caenorhabdi
32	1287.5	30.1	772	5 Q8ERS4	Q8ERS4 manduca sex
33	1277.5	29.8	772	5 Q9BLH1	Q9BLH1 bombyx mori
34	1264	29.5	770	13 Q93394	Q93394 perca flave
35	1208.5	28.2	736	5 Q44857	Q44857 caenorhabdi
36	1204	28.1	749	11 Q35812	Q35812 rattus norv
37	1199.5	28.0	766	5 Q18673	Q18673 caenorhabdi
38	1197	28.0	763	5 Q9XZ01	Q9XZ01 drosophila
39	1168	27.3	816	5 Q8ITZ3	Q8ITZ3 caenorhabdi
40	1137.5	26.6	739	5 Q8T660	Q8T660 venturia ca
41	1096	25.6	787	5 Q9UA44	Q9UA44 aplysia cal
42	972.5	22.7	713	11 Q9E0R2	Q9E0R2 mus musculus
43	945.5	22.1	665	17 Q8TPB2	Q8TPB2 methanocarc
44	937	21.9	754	5 Q19831	Q19831 caenorhabdi
45	934	21.8	694	16 Q8EAQ3	Q8EAQ3 shewanella

## ALIGNMENTS

RESULT 1

ID	Q8NFD7	PRELIMINARY;	PRT;	811 AA.
AC	Q8NFD7			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Endothelin-converting enzyme-2C.			
GN	ECE2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thalamus;			
RA	Punkte-Kaiser H., Scheuch K., Behrouzi T., Synowitz M., Draheim N.,			
RA	Schwaneberg B., Thomas A., Zollmann F.S., Paul M., Orzechowski H.D.;			
RT	"Human endothelin-converting enzyme-2C (ECE-2C): a new ECE-2			
RT	variant."			
RI	Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL, AF521189; AAM7664.1.			
DR	GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.			
DR	GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.			
DR	GO; GO:0008270; F:zinc ion binding; ISS.			
DR	GO; GO:0007420; P:brain development; ISS.			
DR	GO; GO:0010002; P:cardioblast differentiation; ISS.			
DR	GO; GO:0007267; P:cell-cell signaling; ISS.			
DR	GO; GO:0009790; P:embryonic development; ISS.			
DR	GO; GO:0007507; P:heart development; ISS.			
DR	GO; GO:0016486; P:peptide hormone processing; ISS.			
DR	GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.			
DR	GO; GO:0042310; P:vasoconstriction; ISS.			
DR	InterPro; IPR000718; Peptidase_M13.			
DR	InterPro; IPR008753; Peptidase_M13_N.			
DR	InterPro; IPR006025; Pept_M2n_BS.			
DR	InterPro; IPR000221; Protamine_P1.			
DR	Pfam; PF01431; Peptidase_M13; 1.			
DR	Pfam; PF05649; Peptidase_M13_N; 1.			

DR PRINTS; PS00786; NEPRILYSIN.  
DR PROSITE; PS00048; PROTEINASE\_P1; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
SQ SEQUENCE 811 AA; 91211 MW; 7379F7AFEA937FCE CRC64

Query Match	100.0%	Score 4281;	DB 1;	Length 811;
Best Local Similarity	100.0%	Pred. No. 3.4e-301;		
Matches 811; Conservative	0;	Mismatches	0;	Gaps 0

Qy	1	MNVALLQELGASNNWVEYKRALTRDDDAEPTPEVGASPDAMEVGGASPFSPGPGMT	60
Db	1	MNVALLQELGASNNWVEYKRALTRDDDAEPTPEVGASPDAMEVGGASPFSPGPGMT	60
Qy	61	GTPRSSGLFWRTVTCPELRSISGLGSRVWVGPGKTRQLGSRTOLEVLVAGASLLLAALL	120
Db	61	GTPRSSGLFWRTVTCPELRSISGLGSRVWVGPGKTRQLGSRTOLEVLVAGASLLLAALL	120
Qy	121	LGCVLALGVQHRDPDSHSTCLTEACIRVAGKLBESLDKGVSPCEPYPQSPCGGMRIRNPL	180
Db	121	LGCVLALGVQHRDPDSHSTCLTEACIRVAGKLBESLDKGVSPCEPYPQSPCGGMRIRNPL	180
Qy	181	PDGSRNATPMSLWPNQONALIKHLELNTFNSNSEAEOKTORFYLSCLOVERIEELGAPQ	240
Db	181	PDGSRNATPMSLWPNQONALIKHLELNTFNSNSEAEOKTORFYLSCLOVERIEELGAPQ	240
Qy	241	LRDLLEKIGANNITGPMDQDNFMELVKA VAGTYRATPFTVYISADSKSSNSNVIQVDS	300
Db	241	LRDLLEKIGANNITGPMDQDNFMELVKA VAGTYRATPFTVYISADSKSSNSNVIQVDS	300
Qy	301	GLFLPSRDIYLNKRTNKEKYLTYLDYMBELGMLLGGRPSTSTREMOQVLELEIQLANITV	360
Db	301	GLFLPSRDIYLNKRTNKEKYLTYLDYMBELGMLLGGRPSTSTREMOQVLELEIQLANITV	360

Qy	361	PODORDEEKTLYHKMSISELOALASMDLBEFLSFLSLPSELSDESPVYVYGMDLYOOVS	420
Db	361	PODORRDEEKTLYHKMSISELOALASMDLETLSTLSPLSELSDBEPVYVYGMDLYOOVS	420
Qy	421	ELINRTEPSIILNNYLIIMLVOKTSSLDRRPFESAOEKLETLYGTKKS CVPRMOTCISNT	480
Db	421	ELINRTEPSIILNNYLIIMLVOKTSSLDRRPFESAOKLETLYGTKKS CVPRMOTCISNT	480
Qy	481	DDALGFALGSLFVKATPDRQSEIIEGMSIEIRTAFFEEALGOLVMMDEKTRDAALEKADA	540
Db	481	DDALGFALGSLFVKATPDRQSEIIEGMSIEIRTAFFEEALGOLVMMDEKTRDAALEKADA	540
Qy	541	IYDMIGPDPFIIEPEKELDDYDGYEISDSFPQNNLNTYNFSAKMAADOLRKPSPRDOWS	600
Db	541	IYDMIGPDPFIIEPEKELDDYDGYEISDSFPQNNLNTYNFSAKMAADOLRKPSPRDOWS	600
Qy	601	MTPOTVNAVYUPLTKNEIVFPAGIILDAPFYARHHPKALNFGGIGVYMGHELTIAFPDQGRE	660
Db	601	MTPOTVNAVYUPLTKNEIVFPAGIILDAPFYARHHPKALNFGGIGVYMGHELTIAFPDQGRE	660
Qy	661	YDKSGNLRPMMONESLAAFRNHTACMEBOYNOYOUNGERLNGRQTLGENIADNGLKAXY	720
Db	661	YDKSGNLRPMMONESLAAFRNHTACMEBOYNOYOUNGERLNGRQTLGENIADNGLKAXY	720
Qy	721	NAKYMALRKHGEBEOLPAVGLTNHOLFVGFQAOWCSVARTPESSHEGLVTDHPSAPRFRV	780
Db	721	NAKYMALRKHGEBEOLPAVGLTNHOLFVGFQAOWCSVARTPESSHEGLVTDHPSAPRFRV	780
Qy	781	LGTLSNSRDLFRHFGCPVGSPPNNPQOLCEWY 811	
Db	781	LGTLSNSRDLFRHFGCPVGSPPNNPQOLCEWY 811	

RESULT 2	
0865C2	
ID	0865C2
AC	0865C2
DT	01-JUN-2003 (TRENMBLrel. 24, Created)
DT	01-JUN-2003 (TRENMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TRENMBLrel. 25, Last annotation update)

DE Endocheilin-converting enzyme 2b-2.  
OS Bos taurus (Bovine).  
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae  
OC Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
OX

RP SEQUENCE FROM N.A.  
 RA Ikeda S., Emoto N., Aikawa S., Yokoyama M., Matsuo M.,  
 RT "Bovine EGF-2."  
 RL submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AF489576; AAC72353.1;  
 DR GO:0030659; C:cytoplasmic vesicle membrane; ISS.  
 DR GO:0016511; F:endochelin-converting enzyme activity; ISS.  
 DR GO:0008270; F:zinc ion binding; ISS.  
 DR GO:0007420; P:brain development; ISS.  
 DR GO:0010002; P:cardioblast differentiation; ISS.  
 DR GO:0007257; P:cell-cell signaling; ISS.  
 DR GO:0009750; P:embryonic development; ISS.  
 DR GO:0007507; P:heart development; ISS.  
 DR GO:0016486; P:peptide hormone processing; ISS.  
 DR GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.  
 DR GO:0042310; P:vasoconstriction; ISS.  
 DR InterPro, IPR000718; Peptidase\_M3.  
 DR InterPro, IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro, IPR000221; Protamine\_P1.  
 DR Pfam, PF01431; Peptidase\_M3; 1.  
 DR PRINTS, PRO0786; NEPRILYSIN.  
 DR PROSITE, PS00048; PROTAMINE\_P1; 1.  
 DR PROSITE, PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 765 AA; 86243 MW; 12C3BE747881E1FF CMC64;

Query Match	89.2%;	Score 3820;	DB 6;	Length 765;
Best Local Similarity	89.5%;	Pred. No. 7.9e-268;		
Matches 726;	Conservative 17;	Mismatches 22;	Indels 46;	Gaps 1;

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Oy 1 MNVALOEJGASNNVEYKATLRREDAPEPEVEGASDAEVEKGA SPSPGSPGMP 60
Db 1 MRVALOEJGGGNNVEYKATLRREDAPEPEVEGASDAEVE ----- 42
Oy 61 GTPRSSGLFMRVTCPLHRISISGLCSRTWVGFOKOTROLLSGRTOLEVLAGASILLALL 120
Db 43 -----AGFRKTSRLIGHOTLEVLAVGSILLALL 74
Oy 121 LGCIVALGVQHRDPHSHSTCTEACIVAGKILISLRGVPCGDFPOSGGMRRLPL 180
Db 75 LGCIVALGVQHRDPHSHSTCTEACIRVAGKILISLRGVPCGDFPOSGGMRRLPL 134
Oy 181 PDGSRNNTPNLSLMDONALIKHLENTFNSSSEAEKOTRFYLSCLQVERIEELGAQ 240
Db 135 PDGSRNNNSLSLMDONALIKHLENTFPSSSEAEKOTRFYLSCLQVERIEELGNA 194
Oy 241 LRDLIEKIGGNITGPMDDNFMELKAVAGTYATPEFTYVISADSKSSNNVIOVDOS 300
Db 195 LRDLIDKIGGNVYGPMDQDNFMELKAVAGTYATPEFTYVISADSKSSNNIIQVDOS 254
Oy 301 GLFIPSRDYIINRPANKEVLTAYLDYNEELGMLIGRPTSTREOMQVLEIOLANTV 360
Db 255 GLFIPSRDYIINRPANKEVLTAYLDYNEELGMLIGQPTSTREOMQVLEIOLANTV 314
Oy 361 PODORRBEKTYHMSISLQALPMSDMWLEFSLSPLEISDSEPVVYGMVLOQVS 420
Db 315 PODORRBEKTYHMSIAELQALPMSDMWLEFSLSPLEISGSEPVVYGTIYLOQVS 374
Oy 421 ELIRTEPSILANNYLINLVOKTSSLDPRESAQOEKLETLVYTKKSCVPRMOTCISNT 480
Db 375 ELIRTEPSYIANNYLINLVOKTSSLDHRESAQOEKLETLVYTKKSCTRMOTCISNT 434
Oy 481 DDALGFALGSLFVKATPDRQSKIEAEGMISEIRTAFEELAGOLVWMBEKTQAAEKADA 540
Db 435 DDALGFALGSLFVKATPDRQSKIEAEGMISEIRVAFEEALGHLVWMBEKTQAAEKADA 494
Oy 541 IYDMIGPPDPLIEKEKLDVVDGYEISEDSFQNNMLYNFSASVYMDQLAKPSPRDMS 600

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Db 495 IYDMIGFPFIIIEPKELDDYDGYEVSSEDSFQNMNLNLYNFSKAWADQARKPSRDQNS 554
Qy 601 MPTQYNNAYLTPKNEIVPPAGILQAPFYARNHPKALNFGGIVVMGHELTAAFDQGR 660
Db 555 MPTQYNNAYLTPKNEIVPPAGILQAPFYCNHPQALNFGGIVVMGHELTAAFDQGR 614
Qy 661 YDEKGNLRPMWQNESLAAPRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAY 720
Db 615 YDEKGNLRPMWQNESLAAPRNHTACIEBOYSQYQVNGERLNGRQTLGENIADNGLKAAY 674
Qy 721 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVWCSVTRPSSHSGLYTDPHSPARFRY 780
Db 675 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVWCSVTRPSSHSGLYTDPHSPARFRY 734
Qy 781 LGTLSNSRDPILRRFGCPVSGPMNPGQICEVW 811
Db 735 LGTLSNSRDPILRRFGCPVSGPMNPGQICEVW 765

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## RESULT 3

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ID Q865C4 PRELIMINARY; PRT; 816 AA.
AC Q865C4;
DT 01-JUN-2003 (TREMELREL. 24, Created)
DT 01-JUN-2003 (TREMELREL. 25, Last sequence update)
DT 01-OCT-2003 (TREMELREL. 25, Last annotation update)
DE Endothelin-converting enzyme 2a-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Bovine ECE-2a-2.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF489574; AAO72361.1; -.
DR GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0007420; P:brain development; ISS.
DR GO; GO:0010002; P:cardioblast differentiation; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0009790; P:embryonic development; ISS.
DR GO; GO:0007507; P:heart development; ISS.
DR GO; GO:0016486; P:peptide hormone processing; ISS.
DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.
DR GO; GO:0042310; P:vasoconstriction; ISS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000221; Protamine_PL.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00048; PROTAMINE_PL; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 816 AA; 92072 MW; BC0DD8FA062672DE CRC64;

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Query Match 88.1%; Score 3772; DB 6; Length 816;
Best Local Similarity 89.5%; Pred. No. 2.7e-264;
Matches 716; Conservative 18; Mismatches 20; Indels 46; Gaps 1;

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Qy 12 SNMVEKRTALDDEDAPEFVPGASPDAMVKGKASPPSPGSPMTGTPTASSGLFWR 71
Db 63 NEMVEKRTALRDEDAPEFVPGASPDAMVKGKASPPSPGSPMTGTPTASSGLFWR 93
Qy 72 VTCPLHRSISGLCSRTMVGFOKTRQLGSRQLGLVLAGASLLAALLGCVLGVGY 131
Db 94 -----AGFRKRTSLGLGHQLQLVLAGVSLLAALLGCVLGVGY 136
Qy 132 HDPSSHSTCLTRACIRVAKKILLESIDRGVSPCEDFYQSGCGWIRRNPLPDGRSRMNTFN 191

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Db 137 HRDPSSHSTCLTRACIRVAKKILLESIDRGVSPCEDFYQSGCGWIRRNPLPDGRSRMNTFN 196
Qy 192 SIMDQOAILKILLETNTSSSSSEAEQRTQRYLSTQYERIBELGAQOLRDLIEKIGW 251
Db 197 SIMDQOAILKILLETNTSSSSSEAEKRTQRYLSTQYERIBELGAHRLRLIDIKIGW 256
Qy 252 NITGPMDDQNFMEVILKAVAGTRATPEFTVYISADKSSNSNVIOVDSGLFSPSDYL 311
Db 257 NTGPMDDQNFMEVILKAVAGTRATPEFTVYISADKSSNSNVIOVDSGLFSPSDYL 316
Qy 312 NRTANEKVLTAALDYMEELGMLDGRPTSTREMOQVLELEIOLANTVPODRDEKI 371
Db 317 NRTANEKVLTAALDYMEELGMLDGRPTSTREMOQVLELEIOLANTVPODRDEKI 376
Qy 372 YHKMSISELQALAPSDMIEFLSPILSPILSDSEPVVYVYGVNDYIQVSELINRTEPIL 431
Db 377 YHKMSIAELQALAPSDMIEFLSPILSPILSDSEPVVYVYGVNDYIQVSELINRTEPIL 436
Qy 432 NNVLIMNLVQKTTSLDRRFSQAEKLETTYGTYSKSCVPRWQTCISNTDDALGFALGSL 491
Db 437 NNVLIMNLVQKTTSLDRRFSQAEKLETTYGTYSKSCVPRWQTCISNTDDALGFALGSL 496
Qy 492 FYKATFDRQSKELIAGMISEIRTAFAEALGOLVWMDKTRQAKKADAIYDMIGFPDI 551
Db 497 FYKATFDRQSKELIAGMISEIRTAFAEALGOLVWMDKTRQAKKADAIYDMIGFPDI 556
Qy 552 IEPKELDDYDGYEVSSEDSFQNMNLNLYNFSKAWADQARKPSRDQNSMTQYNNAYL 611
Db 557 IEPKELDDYDGYEVSSEDSFQNMNLNLYNFSKAWADQARKPSRDQNSMTQYNNAYL 616
Qy 612 PTKNEIVPPAGILQAPFYARNHPKALNFGGIVVMGHELTAAFDQGRYDEKGNLRPMW 671
Db 617 PTKNEIVPPAGILQAPFYCNHPQALNFGGIVVMGHELTAAFDQGRYDEKGNLRPMW 676
Qy 672 QNESLAAPRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAYNAYKAMLRKHG 731
Db 677 QNESLAAPRNHTACIEBOYSQYQVNGERLNGRQTLGENIADNGLKAAYNAYKAMLRKHG 736
Qy 732 EEOQLPAVGLTNHOLFVYGAQVWCSVTRPSSHSGLYTDPHSPARFRYLGTLNSRDL 791
Db 737 EEOQLPAVGLTNHOLFVYGAQVWCSVTRPSSHSGLYTDPHSPARFRYLGTLNSRDL 796
Qy 792 RHFGCPVSGPMNPGQICEVW 811
Db 797 RHFGCPVSGPMNPGQICEVW 816

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## RESULT 4

```

ID Q923T6 PRELIMINARY; PRT; 763 AA.
AC Q923T6;
DT 01-DEC-2001 (TREMELREL. 19, Created)
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)
DT 01-OCT-2003 (TREMELREL. 25, Last annotation update)
DE Endothelin converting enzyme-2.
GN ECE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Pan H., Zhanavia N., Devi L.A.;
RT "Mouse Endothelin Converting Enzyme-2 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF396699; AAK3919.1; -.
DR MEROPS; M13.003; -.
DR MGD; MGI:1101356; Ece2.
DR GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0007420; P:brain development; IMP.

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DR GO: GO:0010002; P:cardioblast differentiation; IMP.  
 DR GO: GO:0007267; P:cell-cell signaling; ISS.  
 DR GO: GO:0009790; P:embryonic development; ISS.  
 DR GO: GO:0007507; P:heart development; IMP.  
 DR GO: GO:0016486; P:peptide hormone processing; ISS.  
 DR GO: GO:0008277; P:regulation of G-protein coupled receptor pr. . .; ISS.  
 DR GO: GO:0042310; P:vasoconstriction; ISS.  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR008753; Peptidase\_M13\_N.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro: IPR000221; Procamine\_P1.  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR Pfam: PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS: PRO0786; NEPRILysin.  
 DR PROSITE: PS00048; PROTAMINE\_P1; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 763 AA; 86205 MW; 4B518B0E9B549 CRC64;

Query Match 86.3%; Score 3695; DB 11; Length 763;  
 Best Local Similarity 86.6%; Pred. No. 9e-259;  
 Matches 702; Conservative 34; Mismatches 27; Indels 48; Gaps 2;

QY 1 MNVALQELGAGSNMVEYKATLRDEDAPEPTVEGASPDAMEYVGKASPFSPGSPGMP 60  
 DB 1 MNVALHELGGSQMWYKRAKLRDESPETIVEGATRDSLE----- 42

QY 61 GTPRSSGGLFWRYTCPHLRISISGLCSRTWVGFOKGTROLLGSRTOLELVLAGSLIAALL 120  
 DB 43 -----VGFQKRTROLFGSHITOLELVLAGSLIAALL 74

QY 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILLESIDRGVSPEDDYQSPCGMIRNPL 180  
 DB 75 LGCLVALMW--HRDPAHSTCVTEACIRVAKILLESIDRGVSPQDDYQSPCGMIRNPL 132

QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSAEOKTORFYLSCLQVERIEELGAOP 240  
 DB 133 PNRGRSMNTFNSLMDONQAILKHLLENTFNSSSAEOKTRSYLSCLQSERIEKLGAKP 192

QY 241 LRDLIEKIGGWNITGPMODNFMELKAVAGTYRATPFTVYISADSKSNSNVIOVDS 300  
 DB 193 LRDLIKIGGWNITGPMDEDSFMDVYKAVAGTYRATPFTVYVSADSKSNSNVIQVDS 252

QY 301 GLFLPSRDYIANTANEKYLTAIYDYMELGMLGGRPTSTROMQVLELEIOLANTIV 360  
 DB 253 GLFLPSRDYIANTANEKYLTAIYDYMELGVLGQPTSTROMQVLELEIOLANTIV 312

QY 361 POPDRDEEKIYAKMSISELQALAPAMDMLEFLSPLEISDSSEPVVVGMDYLOQVS 420  
 DB 313 POPDRDEEKIYAKMSISELQALAPAVDMLEFLSPLEISDSSEPVVVGTEYLOQVS 372

QY 421 ELINRTEPSTLNNYLIWNLVOKTSSLDRRFESAQKLEFLTYGYKSCVPRMOTCISNT 480  
 DB 373 ELINRTEPSTLNNYLIWNLVOKTSSLDQFFETAQKLEFLTYGYKSCVPRMOTCISNT 432

QY 481 DDALGALGSLIPKATFDSQKEIARGMTSEIRTAPEPALGOLVWMDKTRLOAKKAKA 540  
 DB 433 DDALGALGSLIPKATFDSQKEIARGMTSEIRTAPEPALGOLVWMDKTRLOAKKAKA 492

QY 541 IYDMIGFPDPILEPKELDDVDYEIISDSFFQNMNLNLYNFSKAVADOLRKPSPHDS 600  
 DB 493 IYDMIGFPDPILEPKELDDVDYEIISDSFFQNMNLNLYNFSKAVADOLRKPSPHDS 552

QY 601 MTPQYANAYLLPTKNEIVFPAGILOAPFYARNHPKALNFGIGVNGHEITHAFFDQGB 660  
 DB 553 MTPQYANAYLLPTKNEIVFPAGILOAPFYARNHPKALNFGIGVNGHEITHAFFDQGB 612

QY 661 YXKEGRLRPWKQNESLAFRNHTACMEBOYNOYUNGERLNGRQTLGENIADNGGLKAY 720  
 DB 613 YXDEGRLRPWKQNESLAFRNHTACMEBOYSQYUNGERLNGQLTGENIADNGGLKAY 672

QY 721 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVMCSVTPESSEHGLVTDPHSPPRFV 780  
 DB 673 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVMCSVTPESSEHGLVTDPHSPPRFV 732

QY 781 LGTLNSNRDPLRHFGCPVGSPPNPGOLCEW 811  
 DB 733 LGTLNSNRDPLRHFGCPVGSPPNPGOLCEW 763

RESULT 5  
 Q80257 PRELIMINARY; PRT; 763 AA.  
 AC Q80257;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Endothelin-converting enzyme 2d-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NC NCBL\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;  
 RT "Mouse ECE-2b-2.";  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AR489572; M07235.1; -  
 DR GO: GO:0030659; C:cytoplasmic vesicle membrane; ISS.  
 DR GO: GO:0016511; F:endothelin-converting enzyme activity; ISS.  
 DR GO: GO:0008270; F:zinc ion binding; ISS.  
 DR GO: GO:0007420; P:brain development; ISS.  
 DR GO: GO:0010002; P:cardioblast differentiation; ISS.  
 DR GO: GO:0007267; P:cell-cell signaling; ISS.  
 DR GO: GO:0007900; P:embryonic development; ISS.  
 DR GO: GO:0007507; P:heart development; ISS.  
 DR GO: GO:0016486; P:peptide hormone processing; ISS.  
 DR GO: GO:0008277; P:regulation of G-protein coupled receptor pr. . .; ISS.  
 DR GO: GO:0042310; P:vasoconstriction; ISS.  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro: IPR000221; Procamine\_P1.  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR PRINTS: PRO0786; NEPRILysin.  
 DR PROSITE: PS00048; PROTAMINE\_P1; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 763 AA; 86457 MW; 2AADD31B32CFC1 CRC64;

Query Match 85.6%; Score 3665; DB 11; Length 763;  
 Best Local Similarity 86.1%; Pred. No. 1.3e-256;  
 Matches 698; Conservative 32; Mismatches 33; Indels 48; Gaps 2;

QY 1 MNVALQELGAGSNMVEYKATLRDEDAPEPTVEGASPDAMEYVGKASPFSPGSPGMP 60  
 DB 1 MNVALHELGGSQMWYKRAKLRDESPETIVEGATRDSLE----- 42

QY 61 GTPRSSGGLFWRYTCPHLRISISGLCSRTWVGFOKGTROLLGSRTOLELVLAGSLIAALL 120  
 DB 43 -----VGFQKRTROLFGSHITOLELVLAGSLIAALL 74

QY 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILLESIDRGVSPEDDYQSPCGMIRNPL 180  
 DB 75 LGCLVALMW--HRDPAHSTCVTEACIRVAKILLESIDRGVSPQDDYQSPCGMIRNPL 132

QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSAEOKTORFYLSCLQVERIEELGAOP 240  
 DB 133 PNRGRSMNTFNSLMDONQAILKHLLENTFNSSSAEOKTRSYLSCLQSERIEKLGAKP 192

QY 241 LRDLIEKIGGWNITGPMODNFMELKAVAGTYRATPFTVYISADSKSNSNVIOVDS 300  
 DB 193 LRDLIKIGGWNITGPMDEDSFMDVYKAVAGTYRATPFTVYVSADSKSNSNVIQVDS 252

QY 301 GLFLPSRDYIANTANEKYLTAIYDYMELGMLGGRPTSTROMQVLELEIOLANTIV 360  
 DB 253 GLFLPSRDYIANTANEKYLTAIYDYMELGVLGQPTSTROMQVLELEIOLANTIV 312

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QY 361 PODORDEEKIYHKMSISELQALAPMDWLEFLSLPLELSDSEPPVYVGYMDYLOYS 420
DB 313 PODORDEEKIYHKMSISELQALAPMDWLEFLSLPLELSDSEPPVYVGYMDYLOYS 372
QY 421 ELINTEPESILNNVILWNLVQKTTSSLDRRFSAQKLETLVGTCKSCVPRMOTCISNT 480
DB 373 ELINTEPESILNNVILWNLVQKTTSSLDQRFETAQKLETLVGTCKSCVPRMOTCISNT 432
QY 481 DDALCPALGSLFVKATFDRQSKELAGMTSEIRTAEEELGOLVWMDKETROAKAKA 540
DB 433 DDALCPALGSLFVKATFDRQSKELAGMTSEIRTAEEELGOLVWMDKETROAKAKA 492
QY 541 IYDMIGFPDPILEPKELDDVYGYEISEDSFQNMNLNFSKAWADQRRKPSRQMS 600
DB 493 IYDMIGFPDPILEPKELDDVYGYEISEDSFQNMNLNFSKAWADQRRKPSRQMS 552
QY 601 MTPQVNAVAYLPTKNEIVFPAGILQAPYARNHPKALNFGIGVWGHETLAFDDQRE 660
DB 553 MTPQVNAVAYLPTKNEIVFPAGILQAPYARNHPKALNFGIGVWGHETLAFDDQRE 612
QY 661 YKKEGTLPRMWNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGIKAY 720
DB 613 YKKEGTLPRMWNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGIKAY 672
QY 721 NAYKAWLRKGHEEQOLPAVGLTNHOLFVGFPAQWCVRTPPSSHEGLVTDPHSPARFV 780
DB 673 NAYKAWLRKGHEEQOLPAVGLTNHOLFVGFPAQWCVRTPPSSHEGLVTDPHSPARFV 732
QY 781 LGTLSNSRDLFHRFGCPVSGPMNPQGLCEVW 811
DB 733 LGTLSNSRDLFHRFGCPVSGPMNPQGLCEVW 763

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## RESULT 6

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Q865C3 PRELIMINARY; PRT; 736 AA.
AC Q865C3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2b-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Bovine ECE-2b-1."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL AF489575; AA072362.1; -.
DR GO: GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO: GO:0016511; P:endothelin-converting enzyme activity; ISS.
DR GO: GO:0008270; F:zinc ion binding; ISS.
DR GO: GO:0007420; P:brain development; ISS.
DR GO: GO:0010002; P:cardioblast differentiation; ISS.
DR GO: GO:0007267; P:cell-cell signaling; ISS.
DR GO: GO:0009790; P:embryonic development; ISS.
DR GO: GO:0007507; P:heart development; ISS.
DR GO: GO:0016486; P:peptide hormone processing; ISS.
DR GO: GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.
DR GO: GO:0042310; P:vasoconstriction; ISS.
DR InterPro: IPR000718; Peptidase_M13.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR000221; Proctamine_P1.
DR Pfam: PF01431; Peptidase_M13; 1.
DR PRINTS: PR00786; NEPRILYSIN.
DR PROSITE: PS00048; PROCTAMINE_P1; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 736 AA; 83128 NM; 7ECD124469751D91 CRC64;

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Query Match

85.5%; Score 3659.5; DB 6; Length 736;

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Best Local Similarity 95.3%; Pred. No. 3.2e-256;
Matches 688; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
QY 90 GFQKTRQLGSRTOLELVLAGASLLLAALLGLCVAGVYHRPSSHCTTEACIRVA 149
DB 15 GFRKTRSLGHTLDELVLAVGSLLLAALLGLCVAGVYHRPSSHCTTEACIRVA 74
QY 150 GKILSLRGVSPGSDPFOFSCGWIIRRNPLPDGSRNMTFSLMDONAILKHLENT 209
DB 75 GKILSLRGVSPGSDPFOFSCGWIIRRNPLPDGSRNMTFSLMDONAILKHLENT 134
QY 210 FNSSEAEQKQRFYLSCLQVERIELGAQPLRDLIEKIGWNITGPMQDNFMEVLKAV 269
DB 135 FNSSEAEKQKQRFYLSCLQVERIELGAHRLDILDKIGNNVYGPMDQNFMEVLKAV 194
QY 270 AGTYRATPEFTYVYISADSKSSNSNTIYVDQSLFLPSRDYLNRTANKEVLTAYLDYME 329
DB 195 AGTYRATPEFTYVYISADSKSSNSNTIYVDQSLFLPSRDYLNRTANKEVLTAYLDYME 254
QY 330 LGMLGSRPTSRBOOVLELEIOLANTVPODORDEEKIYHKMSISELQALAPMDW 389
DB 255 LGMLGSGOPTSRBOOVLELEIOLANTVPODORDEEKIYHKMSISELQALAPMDW 314
QY 390 LEFLSLPLELSDSEPPVYVGYMDYLOVSELINRTEPESILNNVILWNLVQKTTSSLD 449
DB 315 LEFLSLPLELSDSEPPVYVGYMDYLOVSELINRTEPESILNNVILWNLVQKTTSSLD 374
QY 450 RFESAQKLETLVGTCKSCVPRMOTCISNTDLAGFALGSLFVATFDRQSKELAGMT 509
DB 375 RFESAQKLETLVGTCKSCVPRMOTCISNTDLAGFALGSLFVATFDRQSKELAGMT 434
QY 510 SEIRTAEEELGOLVWMDKETROAKAKADALYDMIGFPDPILEPKELDDVYGYEISD 569
DB 435 SEIRTAEEELGOLVWMDKETROAKAKADALYDMIGFPDPILEPKELDDVYGYEISD 494
QY 570 SFFQNMNLNFSKAWADQRRKPSRQMSMTPQVNAVAYLPTKNEIVFPAGILQAPY 629
DB 495 SFFQNMNLNFSKAWADQRRKPSRQMSMTPQVNAVAYLPTKNEIVFPAGILQAPY 554
QY 630 ARNHKPALNFGIGVWGHETLAFDDQREYDEKGNLRPMWNESLAFRNHTACMEQ 689
DB 555 TCNHPQALNFGIGVWGHETLAFDDQREYDEKGNLRPMWNESLAFRNHTACMEQ 614
QY 690 YNOYVNGERLNGRQTLGENIADNGIKAAVNAVYAMLRKGHEEQOLPAVGLTNHOLFV 749
DB 615 YNOYVNGERLNGRQTLGENIADNGIKAAVNAVYAMLRKGHEEQOLPAVGLTNHOLFV 674
QY 750 GFAQWCVRTPPSSHEGLVTDPHSPARFVYGLTSLNSRDLFHRFGCPVSGPMNPQGLCE 809
DB 675 GFAQWCVRTPPSSHEGLVTDPHSPARFVYGLTSLNSRDLFHRFGCPVSGPMNPQGLCE 734
QY 810 VW 811
DB 735 VW 736

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## RESULT 7

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Q80259 PRELIMINARY; PRT; 814 AA.
AC Q80259;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 25, Last annotation update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2a-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Mouse ECE-2a-2."

```



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QY 301 GFLPSRDYLRNTANEKVLTAVIDMEELGMLGRPTSTREOMQOVLLEIQLANITV 360
DB 275 GFLPSRDYLRNTANEKVLTAVIDMEELGMLGRPTSTREOMQOVLLEIQLANITV 334
QY 361 PODQDRDEEKIYHKMSISELQALAPSMWLSEFLSPLEISDSSEPVVYVGMVLYQVS 420
DB 335 PODQDRDEEKIYHKMSISELQALAPSMWLSEFLSPLEISDSSEPVVYVGMVLYQVS 394
QY 421 ELINTEPSILNNYLIWNVOKTSSLDLRFESAOKELEIYTGTKSCVPRMOTCISMT 480
DB 395 ELINTEPSILNNYLIWNVOKTSSLDLRFESAOKELEIYTGTKSCVPRMOTCISMT 454
QY 481 DDALGALGSLFVKAFTPDROSKIEAEGMISEIRTAEEALGOLVWMDKTRQAKKADA 540
DB 455 DDALGALGSLFVKAFTPDROSKIEAEGMISEIRTAEEALGOLVWMDKTRQAKKADA 514
QY 541 IYDMIGFPDILPEKELDDVDYGEIISDSFPQNMNLNLYFSKAWADQLRKPSRDQMS 600
DB 515 IYDMIGFPDILPEKELDDVDYGEIISDSFPQNMNLNLYFSKAWADQLRKPSRDQMS 574
QY 601 MTPQYNAAYLPTKNEIVPAGILQAPFPAKRNPKALNFGIGVWGHGELTHAFDQGR 660
DB 575 MTPQYNAAYLPTKNEIVPAGILQAPFPAKRNPKALNFGIGVWGHGELTHAFDQGR 634
QY 661 YKEGNLRPMWONESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGLKAAY 720
DB 635 YKEGNLRPMWONESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGLKAAY 694
QY 721 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVWCVSRTPESSHEGLVTDPHSPARFV 780
DB 695 NAYKAMLRKHGEQOLPAVGLTNHOLFVYGAQVWCVSRTPESSHEGLVTDPHSPARFV 754
QY 781 LGTLSNSRDLRFHFGCPVSGPMNPGQLCEVW 811
DB 755 LGTLSNSRDLRFHFGCPVSGPMNPGQLCEVW 785

RESULT 9
Q80258 PRELIMINARY; PRT; 734 AA.
ID 080258
AC 080258;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2b-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Mouse ECE-2b-1."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AP489571; A072358.1;
DR GO: GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO: GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO: GO:0008270; F:zinc ion binding; ISS.
DR GO: GO:0007420; P:brain development; ISS.
DR GO: GO:0010002; P:cardioblast differentiation; ISS.
DR GO: GO:0007267; P:cell-cell signaling; ISS.
DR GO: GO:0007907; P:embryonic development; ISS.
DR GO: GO:0007507; P:heart development; ISS.
DR GO: GO:0016486; P:regulate hormone processing; ISS.
DR GO: GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.
DR GO: GO:0042310; P:vasoconstriction; ISS.
DR InterPro: IPR000718; Peptidase M13.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR000221; Protamine_P1.
DR Pfam: PF01431; Peptidase M13; 1.
DR PRINTS: PR00786; NEPRILYSIN.
DR PROSITE: PS00048; PROTAMINE_P1; 1.

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DR PROSITE: PS00142; ZINC PROTEASE; 1.
SQ SEQUENCE 734 AA, 83066 MW, 00DAA7AD1F72D5D8 CRC64;
Query Match 83.1%; Score 3556; DB 11; Length 734;
Best Local Similarity 92.7%; Pred. No. 1e-248;
Matches .670; Conservative 26; Mismatches 25; Indels 2; Gaps 1;
QY 89 VGFQKTRQLGSRQLLEVLVAGASILLALGLGLVNLGVQYHDPSPSTCLTEACTIV 148
DB 14 VGFQKTRQLGSRQLLEVLVAGASILLALGLGLVNLGVQYHDPSPSTCLTEACTIV 71
QY 149 AKGILLESIDRGVSPCEDFYQFSCGGMIRRNPLPDGRSRMNTFNSLMDQNALIKHLENT 208
DB 72 AKGILLESIDRGVSPCEDFYQFSCGGMIRRNPLPDGRSRMNTFNSLMDQNALIKHLENT 131
QY 209 TNNSSSEAEQKTQRYFLSCLQVERIBELGAQPLRLIEKIGMNITGPDQDNFMEVLA 268
DB 132 TNNSSSEAEKRTSRFYLSCLOSERIEKLGAKPLRLIDIKIGMNITGPDDEDSFMDVLA 191
QY 269 VAGTYRATPEFTVYISADSKSNSNVIOVDSGLFLPSRDYLRNTANEKVLTAVIDYV 328
DB 192 VAGTYRATPEFTVYISADSKSNSNVITVDQGLFLPSRDYLRNTANEKVLTAVIDYV 251
QY 329 ELGMLLGRPTSTRBOMQOVLLEIQLANITVPQDRDEEKIYHKMSISELQALAPSM 388
DB 252 ELGMLLGRPTSTRBOMQOVLLEIQLANITVPQDRDEEKIYHKMSISELQALAPSM 311
QY 389 WLEFLSPLEISDSSEPVVYVGMVLYQVSELINTEPSILNNYLIWNVOKTSSLD 448
DB 312 WLEFLSPLEISDSSEPVVYVGMVLYQVSELINTEPSILNNYLIWNVOKTSSLD 371
QY 449 RFESAOKELEIYTGTKSCVPRMOTCISMTDDALGALGSLFVKAFTPDROSKIEAEGM 508
DB 372 RFESAOKELEIYTGTKSCVPRMOTCISMTDDALGALGSLFVKAFTPDROSKIEAEGM 431
QY 509 ISEIRTAEEALGOLVWMDKTRQAKKADAIYMGFPDILPEKELDDVDYGEIIS 568
DB 432 ISEIRTAEEALGOLVWMDKTRQAKKADAIYMGFPDILPEKELDDVDYGEIIS 491
QY 569 DSFPQNMNLNLYFSKAWADQLRKPSRDQMSMTQYNAAYLPTKNEIVPAGILQAPF 628
DB 492 DSFPQNMNLNLYFSKAWADQLRKPSRDQMSMTQYNAAYLPTKNEIVPAGILQAPF 551
QY 629 YARNHPKALNFGIGVWGHGELTHAFDQGRDYDEGNLRPMWONESLAFRNHTACME 688
DB 552 YARNHPKALNFGIGVWGHGELTHAFDQGRDYDEGNLRPMWONESLAFRNHTACME 611
QY 689 QYNOYVNGERLNGRQTLGENIADNGLKAAYNAKWLKKGEEQOLPAVGLTNHOLF 748
DB 612 QYNOYVNGERLNGRQTLGENIADNGLKAAYNAKWLKKGEEQOLPAVGLTNHOLF 671
QY 749 VGFQVWCVSRTPESSHEGLVTDPHSPARFVLTGTLNSRDLRFHFGCPVSGPMNPGQL 808
DB 672 VGFQVWCVSRTPESSHEGLVTDPHSPARFVLTGTLNSRDLRFHFGCPVSGPMNPGQL 731
QY 809 EYW 811
DB 732 EYW 734

RESULT 10
Q8C099 PRELIMINARY; PRT; 709 AA.
ID 08C099
AC 08C099;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin converting enzyme-2 homolog.
DE ECE2 OR 6330509A19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

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RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
 RX MEDLINE=2354683; PubMed=1246681;  
 RA The PANTOM Consortium,  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK031951; BAC27618.1; -  
 DR MGD; MGI:1101356; Ece2.  
 DR GO; GO:0030659; Cytoplasmic vesicle membrane; ISS.  
 DR GO; GO:0016511; F-endothelin-converting enzyme activity; ISS.  
 DR GO; GO:0008270; F-zinc ion binding; ISS.  
 DR GO; GO:0007420; P-brain development; ISS.  
 DR GO; GO:0010002; P-cardioblast differentiation; ISS.  
 DR GO; GO:0007267; P-cell-cell signaling; ISS.  
 DR GO; GO:0009790; P-embryonic development; ISS.  
 DR GO; GO:0007507; P-heart development; ISS.  
 DR GO; GO:0016486; P-peptide hormone processing; ISS.  
 DR GO; GO:0008277; P-regulation of G-protein coupled receptor pr. .; ISS.  
 DR GO; GO:0042310; P-vasoconstriction; ISS.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF01431; Peptidase\_M13\_1.  
 DR Pfam; PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 709 AA; 80252 MW; 68815CDDA94C8FA CRC64;

Query Match 78.7%; Score 3371; DB 11; Length 709;

Best Local Similarity 85.5%; Pred. No. 2.4e-235;

Matches 645; Conservative 33; Mismatches 28; Indels 48; Gaps 2;

QY 1 MNVALDELGAGSMVEYKATLTDEDAPEYFGGASPDAMEYGGKASPPSPSGKMP 60  
 DB 1 MNVALHGLGGGSMVEYKAKLDESSPELTIVGKATRSLE----- 42  
 QY 61 GTPRSGLFWRVTCPLHRSISGLCSRTMVGFGKTRQLGSRTOLEVLVAGSLTALL 120  
 DB 43 -----VGFQRTQLGFSHQLLEVLVAGSLTALL 74  
 QY 121 LGGLVALGVQYHDPSSHSTCLTEACIRVAKKILLESIDRGVSPCEDFYVPSGCGMIRNP 180  
 DB 75 LGGLVALMV--HRDPASHSTCVTEACIRVAKKILLESIDRGVSPCEDFYVPSGCGMIRNP 132  
 QY 181 PGRSRKMTNPNLMDONQALIKLLENTTNSSSSEAPQKQRYLSCLQVRIEELGAQ 240  
 DB 133 PGRSRKMTNPNLMDONQALIKLLENTTNSSSSEAPKTRSFYLSCLQSERLEKLGAKP 192  
 QY 241 LRDLIEKIGGMNITGPMDDNFMVYKAVAGTRAPFFTVYISADSKSSNSVIVDGS 300  
 DB 193 LRDLIDKIGGMNITGPMDDNFMVYKAVAGTRAPFFTVYISADSKSSNSVIVDGS 252  
 QY 301 GLFLPSRDYVLRNTANEKVLTAVIDYMEELGMDLGGRPISSTRBQOQVLELITQANIV 360  
 DB 253 GLFLPSRDYVLRNTANEKVLTAVIDYMEELGMDLGGRPISSTRBQOQVLELITQANIV 312  
 QY 361 PQQRARDEEKIYKMGISELQALAPSMDELEFSLSPLELSDSEPVVVVYGMIDYQVS 420  
 DB 313 PQQRARDEEKIYKMGISELQALAPAVDMLEFSLSPLELSDSEPVVVVYGYEYQVS 372  
 QY 421 ELNRTPEPILNNYILNVLVQKTTSLDRFESAQOELELTYGTKKSCVPRQOTCISNT 480  
 DB 373 ELNRTPEPILNNYILNVLVQKTTSLDRFESAQOELELTYGTKKSCVPRQOTCISNT 432  
 QY 481 DDALGVALGSLFYKATFDROSKEIAEGMISEIRTAEBALGOLVMDDEKTRQAKERADA 540  
 DB 433 DDALGVALGSLFYKATFDROSKEIAEGMINEIRSAFETLGLVMDDEKTRLAKEKADA 492  
 QY 541 IYMGIGPDPITLPEKELDYYDGYEISDFPQMLNLNFSKAWADQAKRPSRDWS 600

DB 493 IYDMIGPDPITLPEKELDYYDGYEISDFPQMLNLNFSKAWADQAKRPSRDWS 552  
 QY 601 MTPQTVNAYVYLPKNEIVFPAIGILLQAPFYARNHPKALNFGSIGVVMGHELTAAFDQGRE 660  
 DB 553 MTPQTVNAYVYLPKNEIVFPAIGILLQAPFYARNHPKALNFGSIGVVMGHELTAAFDQGRE 612  
 QY 661 YDKENLRPPWONESLAFRNHTACMEQYQYQYNGSERLNGRQLGENTINDGLKAY 720  
 DB 613 YDKENLRPPWONESLAFRNHTACMEQYQYQYNGSERLNGRQLGENTINDGLKAY 672  
 QY 721 NAYKAMLRKGBEQLPAVGLTNHQLFFVGFPAQV 754  
 DB 673 NAYKAMLRKGBEQLPAVGLTNHQLFFVGFPAQV 706

## RESULT 11

Q9DGN6

PRELIMINARY; PRT: 752 AA.

AC Q9DGN6; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Endothelin converting enzyme-1.

GN ECF-1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

RX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2036360; PubMed=10903177;

RX Takebayashi-Suzuki K., Yanagisawa M., Gourdie R.G., Kanawa N.,

RA Mikawa T.;

RT "In vivo induction of cardiac Purkinje fiber differentiation by

RT coexpression of preproendothelin-1 and endothelin converting enzyme-

RT 1.";

RL Development 127:3523-3532 (2000).

DR EMBL; AF230274; AAF98287.1; -.

DR HSSP; P08473; IDMT.

DR MEROPS; M13.002; -.

DR GO; GO:0016020; P-membrane; IEA.

DR GO; GO:0008237; P-metallopeptidase activity; IEA.

DR GO; GO:004245; F-neprilysin activity; IEA.

DR GO; GO:0008270; F-zinc ion binding; IEA.

DR GO; GO:0006508; P-proteolysis and peptidolysis; IEA.

DR InterPro; IPR000718; Peptidase\_M13.

DR InterPro; IPR008753; Peptidase\_M13\_N.

DR InterPro; IPR006025; Pept\_M\_Zn\_BS.

DR Pfam; PF01431; Peptidase\_M13\_1.

DR Pfam; PF05649; Peptidase\_M13\_N\_1.

DR PRINTS; PR00786; NEPRILYSIN.

DR PROSITE; PS00142; ZINC\_PROTEASE; 1.

SQ SEQUENCE 752 AA; 84985 MW; 386B3DB7BP900656 CRC64;

Query Match 62.0%; Score 2653; DB 13; Length 752;

Best Local Similarity 61.8%; Pred. No. 2.8e-183;

Matches 494; Conservative 112; Mismatches 145; Indels 48; Gaps 5;

QY 14 MVEYRATLRDADAEETPEVGASPDAMEYGGKASPPSPSGKMPGTPRSGLFWRV 73  
 DB 1 MVEYRATLRDADAEETPEVGASPDAMEYGGKASPPSPSGKMPGTPRSGLFWRV 40  
 QY 74 CPHLSISGLCSRTMVGFGKTRQLGSRTOLEVLVAGSLTALLLGCVLGVQYHR 133  
 DB 41 -----AQRTRPKQLVANVAVLAVLGLGLVQYRA 74  
 QY 134 DSHSTCLTEACIRVAKKILLESIDRGVSPCEDFYVPSGCGMIRNPDPGRSRMTNPNL 193  
 DB 75 RPP-AVCISEACISVTSSILSDRTVNPCEDFFSYACGAWKAPPLPDGHSRWGTFNNL 133  
 QY 194 WQONQALHGLLENTTNSSEAPQKQRYLSCLQVRIEELGAQPLDLIEKIGMNI 253



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Db      134 WEHNOQVIMHLENTTANVSSEAEKRYOQACNNESKIEELRAAPLMELIAKLGWNI 193
Qy      254 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYLYNR 313
Db      194 TGPWAGDNNATREYTAHRISSPFSSVYVADSRSKNSNVIQVDSGLFLPSRDYLYNR 253
Qy      314 TANEXVLTVLMEELGMLLGR-PTSTRREQOVLELEIOLANTITVPDORRDEKTY 372
Db      254 TENEXVLTVLMEELGMLLGR-PTSTRREQOVLELEIOLANTITVPDORRDEKTY 313
Qy      373 HKMSISELOALAPSDMWEFLSPLSLDSEPPVYVGYMDYLOQVSELINTEPSIIN 432
Db      314 HKMTAGELKDLPAYVDMPEFLSTVFYVPELNESEPPVYVAKEXYLEQVSDLIATDCKL 373
Qy      433 NYLIWNLVQKTSSLDREPSAOKLELTYGTGKSCVPRMOTCISNTDGLPALGSLF 492
Db      374 NMIMNLVKTSPFLDQFQDAEKKEMEWYGTCKCLPRMKCISDTDNNGLFALGAMF 433
Qy      493 VKATPDROSKELAEGMISIRTAFEELGOLVMMDEKTRQAAKADATYDMIGPDPFL 552
Db      434 VKATPDROSKELAEGMISIRTAFEELGOLVMMDEKTRQAAKADATYDMIGPDPFL 493
Qy      553 EKPELDVYDGYEISDSFQNNMLYNFSAKYMAOQLRKPSPRQDSMTPTVNAAYLP 612
Db      494 DSEKELDKVENDYDAVSDLYFENVMQFYNFSARVTLADQLRKPSPRQDSMTPTVNAAYLP 553
Qy      613 TKNEXVLPAGIIOAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREYDKGNLAPMW 672
Db      554 TKNEXVLPAGIIOAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREYDKGNLAPMW 613
Qy      672 NESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAYNAKMLRKGE 732
Db      614 NESVEFKROTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAYNAKMLRKGE 673
Qy      733 EQOLPAVGLTNHOLFVFGAQCWCVRTPESSHEGLVTPHSPARFVLGTLNSRDLR 792
Db      674 EETLPLGLTNHOLFVFGAQCWCVRTPESSHEGLVTPHSPARFVLGTLNSRDLR 733
Qy      793 HFCGPGSPMNPQOLCEW 811
Db      734 HFCGPGSPMNPQOLCEW 752

RESULT 12
Q7ZTK3 PRELIMINARY; PRT; 752 AA.
AC Q7ZTK3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to endochelin-converting enzyme 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046653; AAH46653.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0004245; F:neprilysin activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01431; Peptidase_M13; I.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 752 AA; 85564 MW; 4BA447B8D3C0F674 CRC64;

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Query Match      60.1%; Score 2574; DB 13; Length 752;
Best Local Similarity 58.9%; Pred. No. 1,5e-177;
Matches 470; Conservative 132; Mismatches 150; Indels 46; Gaps 4;

Qy      14 WVEYKATLRDADAEETPEVGASPDAMEVGKASFPSPGPMGTPTGSRSGLFWRVT 73
Db      1 MSAYKATLRDDEEDVDVSDGEVYENGLOVN-----LRGGRSSGC-W----- 42
Qy      74 CPHLSISGLCSRTWVFOKTRQLLGSRTOLEVLVAGSLIALALLGLVALGVQYHR 133
Db      43 -----SERTHVEKLLVLLVIMSLGLFMSLLALSIOQYN 76
Qy      134 DPHSHCTLEACIRVAGKILSLDRGVSPCEPFOGSCGMRPDPGRSRMTFNSL 193
Db      77 --SNRVLSSECSISTYSSILRSLDSVDCDFQYQSCGMIKGNPVPDGRSRMGTFNSL 134
Qy      194 WDONQALIKHLENTTFFNSSSEAEOKTORFYVLSCLQVERIEELGAQPLDLIETIGWNI 253
Db      135 WEHNOQVIMHLENTTANVSSEAEKRYOQACNNESKIEELRAAPLMELIAKLGWNI 194
Qy      254 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYLYNR 313
Db      195 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYLYNR 254
Qy      314 TANEXVLTVLMEELGMLLGR-PTSTRREQOVLELEIOLANTITVPDORRDEKTY 373
Db      255 TENEXVLTVLMEELGMLLGR-PTSTRREQOVLELEIOLANTITVPDORRDEKTY 314
Qy      374 KMSISELOALAPSDMWEFLSPLSLDSEPPVYVGYMDYLOQVSELINTEPSIIN 433
Db      315 KMTAGELKDLPAYVDMPEFLSTVFYVPELNESEPPVYVAKEXYLEQVSDLIATDCKL 374
Qy      434 YLIWNLVQKTSSLDREPSAOKLELTYGTGKSCVPRMOTCISNTDGLPALGSLFV 493
Db      375 YMMIMNLVKTSPFLDQFQDAEKKELIEMWYGTCKCLPRMKCISDTDNNGLFALGAMF 434
Qy      494 KATPDROSKELAEGMISIRTAFEELGOLVMMDEKTRQAAKADATYDMIGPDPFL 553
Db      435 KATPDROSKELAEGMISIRTAFEELGOLVMMDEKTRQAAKADATYDMIGPDPFL 494
Qy      554 PEKLDVYDGYEISDSFQNNMLYNFSAKYMAOQLRKPSPRQDSMTPTVNAAYLP 613
Db      495 PEKLDVYDGYEISDSFQNNMLYNFSAKYMAOQLRKPSPRQDSMTPTVNAAYLP 554
Qy      614 KNEIVFPAGIIOAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREYDKGNLAPMW 673
Db      555 KNEIVFPAGIIOAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREYDKGNLAPMW 614
Qy      674 ESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAYNAKMLRKGE 733
Db      615 ASVEFKROTACMEBOYNOYQVNGERLNGRQTLGENIADNGLKAAYNAKMLRKGE 674
Qy      734 QOLPAVGLTNHOLFVFGAQCWCVRTPESSHEGLVTPHSPARFVLGTLNSRDLR 793
Db      675 KLPPLGLTNHOLFVFGAQCWCVRTPESSHEGLVTPHSPARFVLGTLNSRDLR 734
Qy      794 FCGPGSPMNPQOLCEW 811
Db      735 FCGPGSPMNPQOLCEW 752

RESULT 13
Q28868 PRELIMINARY; PRT; 758 AA.
AC Q28868;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endochelin converting enzyme.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

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Dd	148	IGHLEENST-ASVSEPERKAQVYYRACMAETRIIEELKAPFLMELIEKGGAMNITGPMDDKD	206
Qy	261	NEMEVILKAVAGTYRATPFEFTYIISADSKSSNSNVIOVDSGLFLPSRDYIANTANAEKYL	320
Dd	207	NFOQDTLQVTVSHYHHSPPFSVYVSADSXSNSNSNVIOVDSGLFLPSRDYIANTANAEKYL	266
Qy	321	TAIYLYMEELGMLLGGRPYST-REMOQVLELEIQLANITVPDODRRDEEKIYHKSISE	379
Dd	267	TGVLNMYMVOGLGLLGGGADITRPQOQIILDFETALANITIPQEKRRDEELIYHKYTAAE	326
Qy	360	LOALAPSMOWIEFLSLFSLPLSEDSPEVYVGMIDLQOVELINTPESLNNYILMNL	439
Dd	327	LOTLPAIWMDFPLNITFYFVEINSESPYITDKLEYLSKVSTLINSIDCKLNNYIMNL	386
Qy	440	VOKTTSILDRRESAOEKLLETLYGKKSCVPEWQTCISNTDAGFALGSLFVKATPDR	499
Dd	367	VKRTSSFLDQRQDADDEKFMENVYGTKKTCLPRMKCVSDTEWTLGFGALGPMVKAITFAE	446
Qy	500	QSKETAEGMISIRTAFEBALGQLYVMDEKTRQAEKADAIYDMIGPDPFIPEYELD	559
Dd	447	DSKNLASEILITIKKAFBESLSTLKKMDDPDKRSAEKADAIYNMIGYPFIMDPKELD	506
Qy	560	YVDGEISDSDFQNMNLNLYNSAKYMAOALRPPSRDQMSMPQVYMYLPTKNEIVP	619
Dd	507	VENDTAVPDLTYFENAMRPFNSWRVTAQULRAAPRDMQSMTPPMWNAYSPTKNEIVP	566
Qy	620	PAGIIQAEFFYANHPKALNFGGIGVVMGHELTHTAFPDQGREYDKENLRPMWNESILAAF	679
Dd	567	PAGIIQAEFFYANHPKALNFGGIGVVMGHELTHTAFPDQGREYDKENLRPMWNESILAAF	626
Qy	660	RNHRTACMEBOYNOYOVNGERLNGRQTLGENIADNGELKAAKYNAKKYKMLRKGEEQOLPAV	739
Dd	627	KQQTACMEBOYNGYNGEVPNGCRHTLGENIADNGELKAAKYRAYQWVKKNGAEQTLPTL	686
Qy	740	GLTNHQLFVVGGAQWCVSVPRESSHEGLVTPHSPARPRVGLTENSNDFLHFGCPVG	799
Dd	667	GLTNHQLFVVGGAQWCVSVPRESSHEGLVTPHSPARPRVGLTENSNDFLHFGCPVG	746
Qy	800	SPMNPGLCEW 811	
Dd	747	SPMNPGLCEW 758	
RESULT 15			
08KOP0			
ID	08KOP0	PRELIMINARY;	PRT; 526 AA.
AC	08KOP0		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)		
DE	Hypothetical protein (Fragment).		
GN	963002SD12RIK OR Bhl27715.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutelesta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RY	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Retina;		
RA	Strausberg R.;		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC030900; AAH30900.1; -		
DR	MGD; MGI:2146683; 963002SD12RIK.		
DR	GO; GO:0016020; C.membrane, IEA.		
DR	GO; GO:0008237; F.membrane, IEA.		
DR	GO; GO:0004245; F.neurilysin activity, IEA.		
DR	GO; GO:0008270; F.zinc ion binding, IEA.		
DR	GO; GO:0006508; P.protein catabolism and peptidolysis, IEA.		
DR	InterPro; IPR000718; Peptidase_M13		
DR	InterPro; IPR008753; Peptidase_M13		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	Pfam; PF01431; Peptidase_M13; 1.		

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DR Pfam: PF05649; Peptidase M13_N; 1.
DR PRINTS; PR00786; NEPRILKSTIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 526 AA; 59939 MW; 326C8BEDC64A51C5 CRC64;

Query Match 55.0%; Score 2352.5; DB 11; Length 526;
Beet Local Similarity 88.2%; Pred. No. 9.4e-162;
Matches 450; Conservative 15; Mismatches 27; Gaps 1

QY 289 SSSNVIVQDSQGLPSRDYLTANTAEKVTAYLDVNEBELGLGGRPTSTREDMQOV 348
Db 1 SSSNVIIQVDSQGLFSPRDYLTANTAEKVTAYLDVNEBELGLGGLGQPTSTREDMQOV 60
QY 349 LLELIQLANITVPQDQRDEEKIYHKMSISELQALAPSDMWLEFLISFLSPLELSDSEPV 408
Db 61 LLELIQLANITVPQQRDEEKIYHKMSISELQALAPAVDMLEFLISFLSPLELSDSEPV 120
QY 409 VVYGYMDYIQOVELNRTPESTLNNYLTWNLYOKTSSIDRFESAOELETLYGTGKS 468
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OY	2161	CGGCTCTGATGAGAGGAACAGTACATCAATACACAGGTCAATGGGAGAGAGGCTCAACGGCC	2220
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OY	2341	ACCACAGACTCTTCTTTCGTGGGATTTGCCCCAGGTGTGTGCTCGGTCCGACACCAAGAGA	2400
Db	2341	ACCACAGACTCTTCTTTCGTGGGATTTGCCCCAGGTGTGTGCTCGGTCCGACACCAAGAGA	2400
OY	2401	GCTCTCAAGAGAGGGGTGGTGAACGACCCCAACAGCCCGCCCGCTCCGAGTCCGAGTGGGCA	2460
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Db	2521	ACCACGGGACGCTGTGTAGAGGTGTGTGAGACCTGTGATCAGGGGAGAAATGCCCCAGCTGTC	2580
OY	2581	ACCAGACCTGGGGGAGAGCTCTCCCTGACAAAGCTGTTTGTCTTGGGTTGGGAGGAAGCAAA	2640
Db	2581	ACCAGACCTGGGGGAGAGCTCTCCCTGACAAAGCTGTTTGTCTTGGGTTGGGAGGAAGCAAA	2640
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OY	2761	TTCACTGTGACATCTTTCCGTGTACACCTCGCTGTGAAAGAGGTCTGTGGGTGGAGAGCAGGT	2820
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OY	3061	TTCACTGACAGCTCTTAATGAGAGCCCAAGGAGCTCTGAAAGAGCTCTGCTGCCACTGT	3120
Db	3061	TTCACTGACAGCTCTTAATGAGAGCCCAAGGAGCTCTGAAAGAGCTCTGCTGCCACTGT	3120
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Db		3121	TTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTACGGGTA CTGTT CCTGTGCTTAGG	3180
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Db		3181	GCACAAGCCTTAGCAAA TGA TTGATTTCCTCGGACAAAGCAGAAGACAGATGAGCAG	3240
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Db		3241	GGAAAAGGAAGAACAGAGTTAATTTTTTACAGAAAAGGGGGTGAGGGTGTGGCTTGGC	33000
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Oy		3361	AAAAAAAAAAAAAAAAAAAA 3377	
Db		3361	AAAAAAAAAAAAAAAAAAAA 3377	
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VERSION				
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TITLE				
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MEDLINE				
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REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
gene				
CDS				





[illegible]

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Qy	3302	CTTATAGGACCCCTGTGCGCAATTAACAGACATGCATCCGTC	33411
Db	3189	CTTATAGGACCCCTGTGCGCAATTAACAGACATGCATCCGTC	3228

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
AF192531	Homo sapiens endothelin-converting enzyme 2B (ECE2) cds; alternatively spliced.	AF192531	GI:11065939	
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3138) Lorenzo,M.N., Khan,R.Y., Wang,Y., Tai,S.C., Chan,G.C., Cheung,A.H. and Marsden,P.A. Human endothelin converting enzyme-2 (ECE2): characterization of RNA species and chromosomal localisation Biochim. Biophys. Acta 1522 (1), 46-52 (2001)			
TITLE	Journal MEDLINE PUBMED AUTHORS	21573691 11718899		
JOURNAL	2 (bases 1 to 3138) Lorenzo,M.-N., Wang,Y., Tai,S.C., Chan,G.C., Khan,R.Y., Cheung,A.H. and Marsden,P.A. Direct Submission Submitted (06-OCT-1999) Medicine, University of Toronto, Rm 7358 Medical Sciences Building, 1 King's College Circle, Toronto, Ontario M5S 1A8, Canada Location/Qualifiers			
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Db	1963	TGCATGAGAGAA	CACATACATCAATCAATACCAGGCTCAATGGGAGAGAGGCTCAAGCGCGCAG	2022	
QY	2226	ACGCTGGGGAGAA	CATTGCTTGACAA	CGGGGGGCTGAAAGGCTGCTTACATGCTTTACAA	2285
Db	2023	ACGCTGGGGAGAA	CATTGCTTGACAA	CGGGGGGCTGAAAGGCTGCTTACATGCTTTACAA	2082
QY	2286	GCATGGCTTGAA	AAACATGGGGAGAGACGACCTGCGGGCTCAACCAAC	2345	
Db	2083	GCATGGCTTGAA	AAACATGGGGAGAGACGACCTGCGGGCTCAACCAAC	2142	
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Db 3443 AGGAGAAACAGAGCTTTATTTTTTACAGAAAAGAGGGTGGAGAGGGTGGTCTTGGCCCTTA 3102

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RESULT	4
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LOCUS	
DEFINITION	3410 bp mRNA linear PRI 11-JAN-2002
ACCESSION	Homo sapiens endothelein converting enzyme-2A (ECE2) mRNA, complete cds; alternatively spliced.
VERSION	AF428263
KEYWORDS	AF428263.1 GI:16903012
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
1 (pages 1 to 3410)  
Lorenzo, M. N., Khan, R. Y., Wang, Y., Tai, S. C., Chan, G. C., Cheung, A. H.  
AUTHORS  
TITLE  
Human endothelin converting enzyme-2 (ECE2): characterization of  
mRNA species and chromosomal localization  
JOURNAL  
Biochem. Biophys. Acta 1522 (1), 46-52 (2001)  
MEDLINE  
21575691

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 3410)  
Lorenzo, M.-N., Khan, R. Y., Wang, Y., Tai, S. C., Chan, G. C., Cheung, A. H.  
and Marden, P. A.  
Direct Submission  
Submitted (05-OCT-2001) Medicine, University of Toronto, 1 King's  
College Circle Rm. 7358, Toronto, Ontario M5S1A8, Canada

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VERSION AF428264.1 GI:16903014  
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SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Lorenzo, M.N., Khan, R.Y., Wang, Y., Tai, S.C., Chan, G.C., Cheung, A.H.  
and Marsden, P.A.  
TITLE Human endothelin converting enzyme-2 (ECE2): characterization of  
mRNA species and chromosomal localization  
JOURNAL Biochim. Biophys. Acta 1522 (1), 46-52 (2001)  
MEDLINE 21575691  
PUBMED 11718899  
REFERENCE 2 (bases 1 to 3051)  
AUTHORS Lorenzo, M.-N., Khan, R. Y., Wang, Y., Tai, S. C., Chan, G. C., Cheung, A. H.

and Marsden, P.A.  
Direct Submission  
Submitted (05-OCT-2001) Medicine, University of Toronto, 1 King's  
College Circle Rm. 7358, Toronto, Ontario M5S1A8, Canada  
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ACCESSION BD248425.1 GI:33058195  
VERSION JP 2002525039-A/1.  
KEYWORDS JP 2002525039-A/1.  
SOURCE Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 3000)  
AUTHORS Walker, M.G., Volkmut, W. and Klingler, T.M.  
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JOURNAL Patent: JP 2002525039-A/1 13-AUG-2002;  
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VERSION  
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Funke-Kaiser, H., Scheuch, K., Behrouzi, T., Synowitz, M., Draheim, N., Schwaneberg, B., Thomas, A., Zollmann, F. S., Paul, M., and Orzechowski, H. D.  
Human endothelin-converting enzyme-2C (ECE-2C): a new ECE-2 variant  
TITLE  
Unpublished  
JOURNAL  
2 (bases 1 to 2667)  
Funke-Kaiser, H., Scheuch, K., Behrouzi, T., Synowitz, M., Draheim, N., Schwaneberg, B., Thomas, A., Zollmann, F. S., Paul, M., and Orzechowski, H. D.  
Direct Submission  
JOURNAL  
Submitted (13-JUN-2002) Clinical Pharmacology and Toxicology, Benjamin Franklin Medical Center, Freie Universitat Berlin, Hindenburgdamm 30, Berlin 12200, Germany  
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Location/Qualifiers



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REFERENCE  
1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
Guiney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.R. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
JOURNAL The same  
PATENT Patent: WO 0168848-A 419 20-SEP-2001;  
Genentech, Inc. (US)  
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TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
JOURNAL A Bioinformatics Assessment  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 2602)  
AUTHORS Clark, H.P.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAY-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

Query Match	Best Local Similarity	72.9%; Score 2461.2; DB 9; Length 2602;
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;		
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 3291)  
Ikeda, S., Emoto, N., Ikeda, K., Yokoyama, M. and Matsuo, M.  
Direct Submission  
Submitted (01-MAR-2002) Division of Molecular Medicine,  
International Center for Medical Research, Kobe University Graduate  
School of Medicine, 7-5-1, Kusunoki, Chuo, Kobe 6500017, Japan  
Location/Qualifiers  
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ORIGIN

Query Match 64.2%; Score 2169.6; DB 4; Length 3291;  
Best Local Similarity 85.3%; Pred. No. 0;  
Matches 2560; Conservative 0; Mismatches 404; Indels 38; Gaps 11;

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Matsuo, M.  
Bovine ECE-2b-2  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 3171)  
AUTHORS Ikeda, S., Emoto, N., Aikawa, J., Ikeda, K., Yokoyama, M. and  
Matsuo, M.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAR-2002) Division of Molecular Medicine,  
International Center for Medical Research, Kobe University Graduate  
School of Medicine, 7-5-1, Kusunoki, Chuo, Kobe 6500017, Japan  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 20:09:01 ; Search time 73 Seconds

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43	3824.5	89.3	736	12	US-10-201-853-420	Sequence 420, App
44	3824.5	89.3	736	12	US-10-013-917A-526	Sequence 526, App
45	3824.5	89.3	736	12	US-10-174-581-420	Sequence 420, App

## ALIGNMENTS

RESULT 1  
US-10-267-502-253  
; Sequence 253, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267, 502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 253  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-267-502-253

Query Match	100.0%	Score 4281	DB 12	Length 811
Best Local Similarity	100.0%	Pred. No. 0		
Matches 811	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MNVALGELGAGSNMVEYKRA	12	US-10-267-502-253
DB	1	MNVALGELGAGSNMVEYKRA	14	US-10-273-992-2
QY	61	GTPRRSGGLFWRYTCPLIRISISGICSTWVGFGQKTRQLLGSRTQLLELYLAGASLLAALL	120	
DB	61	GTPRRSGGLFWRYTCPLIRISISGICSTWVGFGQKTRQLLGSRTQLLELYLAGASLLAALL	120	
QY	121	LGCTVALGQYRDPSHSTCTFEACIRVAGKILIESIDRGVSPCEPDYQSPCGMIRNP	180	
DB	121	LGCTVALGQYRDPSHSTCTFEACIRVAGKILIESIDRGVSPCEPDYQSPCGMIRNP	180	
QY	181	PDGRSMTNFNSIMDNOAILKRLLENTFNSSEBAOKTORFYISCLQVERIEBELGAOP	240	
DB	181	PDGRSMTNFNSIMDNOAILKRLLENTFNSSEBAOKTORFYISCLQVERIEBELGAOP	240	



QY 241 LRDLEKIGGMNITGPMDDNFMENVLKAAGTYRATPFYVYISADSKSSNVIOVDS 300  
DB 241 LRDLEKIGGMNITGPMDDNFMENVLKAAGTYRATPFYVYISADSKSSNVIOVDS 300  
QY 301 GLPLSRDYLLNRTANEKVLTAVIDYMEELGMLGGPSTREBOMQVLELEIOLANTIV 360  
DB 301 GLPLSRDYLLNRTANEKVLTAVIDYMEELGMLGGPSTREBOMQVLELEIOLANTIV 360  
QY 361 PQRDRDEEKIYHKMSISELOALAPSDMWLEFLSLPLSLSDSEPVVYVGYMDYLOQVS 420  
DB 361 PQRDRDEEKIYHKMSISELOALAPSDMWLEFLSLPLSLSDSEPVVYVGYMDYLOQVS 420  
QY 421 ELINRTEPSILNNYLLIMLVQKTTSLDRPFESAQEKLETLVGTCKSCVPMQTCISNT 480  
DB 421 ELINRTEPSILNNYLLIMLVQKTTSLDRPFESAQEKLETLVGTCKSCVPMQTCISNT 480  
QY 481 DDALGFALGSLFYKATFDRQSKIEAGMISEIRTAPEALGOLVMMDEKTRQAKEKADA 540  
DB 481 DDALGFALGSLFYKATFDRQSKIEAGMISEIRTAPEALGOLVMMDEKTRQAKEKADA 540  
QY 541 IYDMIGPDPFLEPKELDDVDYGEISEDSFQNMMLNLFNSAKVADQLRKPSRDWS 600  
DB 541 IYDMIGPDPFLEPKELDDVDYGEISEDSFQNMMLNLFNSAKVADQLRKPSRDWS 600  
QY 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARHHPKALNPGGIGVWGHLELTHAFDQGRE 660  
DB 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARHHPKALNPGGIGVWGHLELTHAFDQGRE 660  
QY 661 YDKEGNLRPMWONESLAAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAA 720  
DB 661 YDKEGNLRPMWONESLAAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAA 720  
QY 721 NAYKAWLRKHGEEOQLPAVGLTNHQLFVGFPAQVCSVTPRESSHEGLVTDPHSPARFRV 780  
DB 721 NAYKAWLRKHGEEOQLPAVGLTNHQLFVGFPAQVCSVTPRESSHEGLVTDPHSPARFRV 780  
QY 781 LGTLSNSRDLRHFPGCPVSPMNPQGLCEW 811  
DB 781 LGTLSNSRDLRHFPGCPVSPMNPQGLCEW 811

RESULT 2  
US-10-273-992-2  
; Sequence 2, Application US/10273992  
; Publication No. US20030129700A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: C1001200DIV  
; CURRENT APPLICATION NUMBER: US/10/273.992  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Human  
US-10-273-992-2

Query Match 100.0%; Score 4281; DB 14; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNVALDELGAGSNMVEYKATLRDEDEAPETPVEGASPDAMEYKGSPPSPGSPMP 60  
DB 1 MNVALDELGAGSNMVEYKATLRDEDEAPETPVEGASPDAMEYKGSPPSPGSPMP 60  
QY 61 GTPRSSGGLFRRVTCPHIRISISGLCSRTMVGFOKTRQLLSRQLDELIVLAGASILLALL 120  
DB 61 GTPRSSGGLFRRVTCPHIRISISGLCSRTMVGFOKTRQLLSRQLDELIVLAGASILLALL 120

QY 121 LGCLVALGQYHRDPESHSTCLTEACIRVAGKILIESLDRGVSPCEDFYQSCGMIIRBNPL 180  
DB 121 LGCLVALGQYHRDPESHSTCLTEACIRVAGKILIESLDRGVSPCEDFYQSCGMIIRBNPL 180  
QY 181 PGRSRMNTFNSLMDONQALILHLENTTFNSSSEABQKTRFPYLSCLQVERIEELGAOP 240  
DB 181 PGRSRMNTFNSLMDONQALILHLENTTFNSSSEABQKTRFPYLSCLQVERIEELGAOP 240  
QY 241 LRDLEKIGGMNITGPMDDNFMENVLKAAGTYRATPFYVYISADSKSSNVIOVDS 300  
DB 241 LRDLEKIGGMNITGPMDDNFMENVLKAAGTYRATPFYVYISADSKSSNVIOVDS 300  
QY 301 GLPLSRDYLLNRTANEKVLTAVIDYMEELGMLGGPSTREBOMQVLELEIOLANTIV 360  
DB 301 GLPLSRDYLLNRTANEKVLTAVIDYMEELGMLGGPSTREBOMQVLELEIOLANTIV 360  
QY 361 PQRDRDEEKIYHKMSISELOALAPSDMWLEFLSLPLSLSDSEPVVYVGYMDYLOQVS 420  
DB 361 PQRDRDEEKIYHKMSISELOALAPSDMWLEFLSLPLSLSDSEPVVYVGYMDYLOQVS 420  
QY 421 ELINRTEPSILNNYLLIMLVQKTTSLDRPFESAQEKLETLVGTCKSCVPMQTCISNT 480  
DB 421 ELINRTEPSILNNYLLIMLVQKTTSLDRPFESAQEKLETLVGTCKSCVPMQTCISNT 480  
QY 481 DDALGFALGSLFYKATFDRQSKIEAGMISEIRTAPEALGOLVMMDEKTRQAKEKADA 540  
DB 481 DDALGFALGSLFYKATFDRQSKIEAGMISEIRTAPEALGOLVMMDEKTRQAKEKADA 540  
QY 541 IYDMIGPDPFLEPKELDDVDYGEISEDSFQNMMLNLFNSAKVADQLRKPSRDWS 600  
DB 541 IYDMIGPDPFLEPKELDDVDYGEISEDSFQNMMLNLFNSAKVADQLRKPSRDWS 600  
QY 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARHHPKALNPGGIGVWGHLELTHAFDQGRE 660  
DB 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARHHPKALNPGGIGVWGHLELTHAFDQGRE 660  
QY 661 YDKEGNLRPMWONESLAAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAA 720  
DB 661 YDKEGNLRPMWONESLAAFRNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAA 720  
QY 721 NAYKAWLRKHGEEOQLPAVGLTNHQLFVGFPAQVCSVTPRESSHEGLVTDPHSPARFRV 780  
DB 721 NAYKAWLRKHGEEOQLPAVGLTNHQLFVGFPAQVCSVTPRESSHEGLVTDPHSPARFRV 780  
QY 781 LGTLSNSRDLRHFPGCPVSPMNPQGLCEW 811  
DB 781 LGTLSNSRDLRHFPGCPVSPMNPQGLCEW 811

RESULT 3  
US-09-888-615-80  
; Sequence 80, Application US/09888615  
; Patent No. US20020064856A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOMMAN, GREGORY  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: CAENEPEEL, SEAN  
; APPLICANT: CHARYDCZAK, GLEN  
; APPLICANT: MANNING, GERRARD  
; TITLE OF INVENTION: NOVEL PROTEASES  
; FILE REFERENCE: 038602/1214  
; CURRENT APPLICATION NUMBER: US/09/888.615  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: 60/214,047  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 80  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Homo sapiens



US-09-888-615-80

Query Match 93.3%; Score 3993; DB 9; Length 765;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

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QY 1 MNVALDELGAGSNMVEYKRALTRDEDAPEPVEGASPDAMEVGKASPPSPGMP 60
DB 1 MNVALDELGAGSNMVEYKRALTRDEDAPEPVEGASPDAMEVGKASPPSPGMP 60
QY 61 GTPRSSGLFWRVYCPHLRSISGLCSRTMWGFOKTRQLLSRTQLLELVLAGASILLALL 120
DB 43 -----VFQKGTQLLSRTQLLELVLAGASILLALL 74
QY 121 LGCLVALGYQYHRDPESHSTCLTEACTRVAKKILIESIDRGVSPCEDFYQSPCGWIRRNPL 180
DB 75 LGCLVALGYQYHRDPESHSTCLTEACTRVAKKILIESIDRGVSPCEDFYQSPCGWIRRNPL 134
QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORPYLSCLOVERIEELGAOP 240
DB 135 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORPYLSCLOVERIEELGAOP 194
QY 241 LRDLEIKIGMNTTGMWDQNFMEVLKAVAGTYRATPFTVYISADSKSNSVIOVDOS 300
DB 195 LRDLEIKIGMNTTGMWDQNFMEVLKAVAGTYRATPFTVYISADSKSNSVIOVDOS 254
QY 301 GLFLPSRDYILNRTANKEKYLTAFLDYMEELGMLGSRPTSTREMOQVLELEIOLANITY 360
DB 255 GLFLPSRDYILNRTANKEKYLTAFLDYMEELGMLGSRPTSTREMOQVLELEIOLANITY 314
QY 361 PODORDEEKIYHKMSISELOALAPSMDLFLSLPLSLSDSEPVVYVGYNDYIQOVS 420
DB 315 PODORDEEKIYHKMSISELOALAPSMDLFLSLPLSLSDSEPVVYVGYNDYIQOVS 374
QY 421 ELINRTEPSILNNYILMNLVQKTTSLDRPFESAQOKLETLYGTYKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNYILMNLVQKTTSLDRPFESAQOKLETLYGTYKSCVPRMOTCISNT 434
QY 481 DDALGFALGSLFVKATFDRQSKIEAGMISEIRTAEEALGOLVMMDEKTRQAKKAKADA 540
DB 435 DDALGFALGSLFVKATFDRQSKIEAGMISEIRTAEEALGOLVMMDEKTRQAKKAKADA 494
QY 541 IYDMIGFPDPILEPKELDLDVYGEI SEDSFQNMMLNLYNFAKVMADOLRRPSSDQNS 600
DB 495 IYDMIGFPDPILEPKELDLDVYGEI SEDSFQNMMLNLYNFAKVMADOLRRPSSDQNS 554
QY 601 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHEITHAFFDQGRE 660
DB 555 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHEITHAFFDQGRE 614
QY 661 YKEGRLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGILKAAY 720
DB 615 YKEGRLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGILKAAY 674
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWC SVTPSSHEGLVTDPHSPARFRV 780
DB 675 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWC SVTPSSHEGLVTDPHSPARFRV 734
QY 781 LGTILNSRDFLRHFGCPVGS PMNPGOLCEVW 811
DB 735 LGTILNSRDFLRHFGCPVGS PMNPGOLCEVW 765
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RESULT 4  
US-10-273-992-4

; Sequence 4, Application US/10273992

; Publication No. US20030129700A1

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al.

; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

; FILE REFERENCE: CL001200DIV

CURRENT APPLICATION NUMBER: US/10/273,992

; CURRENT FILING DATE: 2002-10-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 765

; TYPE: PR

; ORGANISM: Human

US-10-273-992-4

Query Match 93.3%; Score 3993; DB 14; Length 765;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

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QY 1 MNVALDELGAGSNMVEYKRALTRDEDAPEPVEGASPDAMEVGKASPPSPGMP 60
DB 1 MNVALDELGAGSNMVEYKRALTRDEDAPEPVEGASPDAMEVGKASPPSPGMP 42
QY 61 GTPRSSGLFWRVYCPHLRSISGLCSRTMWGFOKTRQLLSRTQLLELVLAGASILLALL 120
DB 43 -----VFQKGTQLLSRTQLLELVLAGASILLALL 74
QY 121 LGCLVALGYQYHRDPESHSTCLTEACTRVAKKILIESIDRGVSPCEDFYQSPCGWIRRNPL 180
DB 75 LGCLVALGYQYHRDPESHSTCLTEACTRVAKKILIESIDRGVSPCEDFYQSPCGWIRRNPL 134
QY 181 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORPYLSCLOVERIEELGAOP 240
DB 135 PDGRSMNTFNSLMDONQAILKHLLENTFNSSSEAOQTORPYLSCLOVERIEELGAOP 194
QY 241 LRDLEIKIGMNTTGMWDQNFMEVLKAVAGTYRATPFTVYISADSKSNSVIOVDOS 300
DB 195 LRDLEIKIGMNTTGMWDQNFMEVLKAVAGTYRATPFTVYISADSKSNSVIOVDOS 254
QY 301 GLFLPSRDYILNRTANKEKYLTAFLDYMEELGMLGSRPTSTREMOQVLELEIOLANITY 360
DB 255 GLFLPSRDYILNRTANKEKYLTAFLDYMEELGMLGSRPTSTREMOQVLELEIOLANITY 314
QY 361 PODORDEEKIYHKMSISELOALAPSMDLFLSLPLSLSDSEPVVYVGYNDYIQOVS 420
DB 315 PODORDEEKIYHKMSISELOALAPSMDLFLSLPLSLSDSEPVVYVGYNDYIQOVS 374
QY 421 ELINRTEPSILNNYILMNLVQKTTSLDRPFESAQOKLETLYGTYKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNYILMNLVQKTTSLDRPFESAQOKLETLYGTYKSCVPRMOTCISNT 434
QY 481 DDALGFALGSLFVKATFDRQSKIEAGMISEIRTAEEALGOLVMMDEKTRQAKKAKADA 540
DB 435 DDALGFALGSLFVKATFDRQSKIEAGMISEIRTAEEALGOLVMMDEKTRQAKKAKADA 494
QY 541 IYDMIGFPDPILEPKELDLDVYGEI SEDSFQNMMLNLYNFAKVMADOLRRPSSDQNS 600
DB 495 IYDMIGFPDPILEPKELDLDVYGEI SEDSFQNMMLNLYNFAKVMADOLRRPSSDQNS 554
QY 601 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHEITHAFFDQGRE 660
DB 555 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHEITHAFFDQGRE 614
QY 661 YKEGRLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGILKAAY 720
DB 615 YKEGRLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGILKAAY 674
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWC SVTPSSHEGLVTDPHSPARFRV 780
DB 675 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWC SVTPSSHEGLVTDPHSPARFRV 734
QY 781 LGTILNSRDFLRHFGCPVGS PMNPGOLCEVW 811
DB 735 LGTILNSRDFLRHFGCPVGS PMNPGOLCEVW 765
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RESULT 5

US-10-453-764-2

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; Sequence 2, Application US/10453764
; Publication No. US20030232044A1
; GENERAL INFORMATION:
; APPLICANT: White, David
; TITLE OF INVENTION: USE FOR ENDOTHELIN CONVERTING ENZYME 2
; TITLE OF INVENTION: (ECC-2) IN THE DIAGNOSIS AND TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: MP102-266P1RM
; CURRENT APPLICATION NUMBER: US/10/453,764
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 60/386,333
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-453-764-2

Query Match      93.3%; Score 3993; DB 15; Length 765;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

QY      1  MNVALDELGASNMVEYKATLRDEDAPEPTVEGASPDAMEYKGSPPSPGMP 60
DB      1  MNVALDELGASNMVEYKATLRDEDAPEPTVEGASPDAMEYKGSPPSPGMP 42
QY      61  GTPRSSGLFWRVTCPLRLSISGLCSRTWVGFKQTRQLGSRQLQLEIVLAGSLIAALL 120
DB      43  -----VFQKQTRQLGSRQLQLEIVLAGSLIAALL 74
QY      121  LGGLVALGVQYHRDPSSHSTCLTEACTRVACKTIIESLDRGVSPCEDPFGSCGMIRNPL 180
DB      75  LGGLVALGVQYHRDPSSHSTCLTEACTRVACKTIIESLDRGVSPCEDPFGSCGMIRNPL 134
QY      181  PDGRSMMNTFNSLMDONQALIKHLLENTFNSSSEAEQKQRYLSCLQYERIEELGAOP 240
DB      135  PDGRSMMNTFNSLMDONQALIKHLLENTFNSSSEAEQKQRYLSCLQYERIEELGAOP 194
QY      241  LRDLIEKIGMNTGPDQDNFMEVLKAVAGYRATPFTFYISADSKSSNSVIOVDOS 300
DB      195  LRDLIEKIGMNTGPDQDNFMEVLKAVAGYRATPFTFYISADSKSSNSVIOVDOS 254
QY      301  GLFLPRDYYLNTANEKUYTAYLDVNEELGMLGGPSTREMOQVLELQIANITY 360
DB      255  GLFLPRDYYLNTANEKUYTAYLDVNEELGMLGGPSTREMOQVLELQIANITY 314
QY      361  PDQRDEDEKIYHKMSISELQALAPSMWLEFLSFLSPLELSDSEPVVYVYGMVYLOQVS 420
DB      315  PDQRDEDEKIYHKMSISELQALAPSMWLEFLSFLSPLELSDSEPVVYVYGMVYLOQVS 374
QY      421  ELINRTEPSILNNYLIWNLVQKTTSSIDRRPESAOEKLFTLYGTXKSCVPRMOTCISNT 480
DB      375  ELINRTEPSILNNYLIWNLVQKTTSSIDRRPESAOEKLFTLYGTXKSCVPRMOTCISNT 434
QY      481  DDALGFLGSLFVKATPDROSKELAEEMISEIRTAPEALGOVMMDEKROAKEXADA 540
DB      435  DDALGFLGSLFVKATPDROSKELAEEMISEIRTAPEALGOVMMDEKROAKEXADA 494
QY      541  IYDMIGPDLILPEKELDYDGEIASEDSFFQNMMLLYNFSKAVMAOQLRKPSRDQMS 600
DB      495  IYDMIGPDLILPEKELDYDGEIASEDSFFQNMMLLYNFSKAVMAOQLRKPSRDQMS 554
QY      601  MTPQTVNAYYLLPTKNEIIVPAGILQAFYARNHPKALNFGSIGVVMGHELTAAFDQGRE 660
DB      555  MTPQTVNAYYLLPTKNEIIVPAGILQAFYARNHPKALNFGSIGVVMGHELTAAFDQGRE 614
QY      661  YDEKGNLRPWWONESLAFRNHTACMEEOYNOYOVNERLINGQTLGENTADNGGLKAA 720
DB      615  YDEKGNLRPWWONESLAFRNHTACMEEOYNOYOVNERLINGQTLGENTADNGGLKAA 674
QY      721  NAYKAWLRKGEEQQLPAVGLTNHQLFVGFPAQVWCVTPRESSHEGLVTDPSPARFRV 780
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DB      675  NAYKAWLRKGEEQQLPAVGLTNHQLFVGFPAQVWCVTPRESSHEGLVTDPSPARFRV 734
QY      781  LGTLSNRDPLRHFQCPVGSPPNNPQOLCEW 811
DB      735  LGTLSNRDPLRHFQCPVGSPPNNPQOLCEW 765

RESULT 6
US-09-978-295A-526
; Sequence 526, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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74 AKKILESIDRGVSPCEDFYQSCGWMIRRNPLPDGRSRMNTFNSLMDQNALIKHLLENT 133  
209 TNNSSSEABQKQRFYSLCLQVERIBELGAOPLRDLIEKIGMNTGPMQDNFMEVLKA 268  
134 TNNSSSEABQKQRFYSLCLQVERIBELGAOPLRDLIEKIGMNTGPMQDNFMEVLKA 193  
269 VAGTRATPFYTYISADSKSSNSVIOVDQSLPLPSRDYILNRTANKVLTAYLDYME 328  
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APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferreira, Napoleon  
APPLICANT: Filvaroff, Ellen  
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APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
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APPLICANT: Wood, William I.  
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; Patent No. US20020177553A1
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; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerltsen, Mary E.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 9; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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14 VGFQKGTROLLGSRTOLEVLVAGASILLALLLGLCVLGVQYHRDPHSHTCLTEACIRV 73  
QY 149 AGKILESLDRGVSPCCDFYQFSCGWIIRRNPLPDGSRNMTFMSLDQNALIKHLENT 208  
74 AGKILESLDRGVSPCCDFYQFSCGWIIRRNPLPDGSRNMTFMSLDQNALIKHLENT 133  
QY 209 TFFSSSEAEOKTORFLYSLCLOVERISELAQPLRDLIEKIGGNITGPMODQFMETLKA 268  
134 TFFSSSEAEOKTORFLYSLCLOVERISELAQPLRDLIEKIGGNITGPMODQFMETLKA 193  
QY 269 VAGTYRATPEFTYIISADSKSSNSNVIQVDQGLFLPSRDYILNRITANEKVLTAIADYME 328  
194 VAGTYRATPEFTYIISADSKSSNSNVIQVDQGLFLPSRDYILNRITANEKVLTAIADYME 253  
QY 329 ELGMLIGRPTSTREMOQVLELEIOLANITYPQDRDBEKKYHKMSISELOALAPSM 388  
254 ELGMLIGRPTSTREMOQVLELEIOLANITYPQDRDBEKKYHKMSISELOALAPSM 313  
QY 389 WLEFLSFLSPLEISDSEPVVYGMVYLOQVSELINRTEPSILNNYILNNLVOKTSSLD 448  
314 WLEFLSFLSPLEISDSEPVVYGMVYLOQVSELINRTEPSILNNYILNNLVOKTSSLD 373  
QY 449 RRESAOKELLETLYGTKSCVPRWOTCISNTDDALGFALGSLFVATPDROSKETAEQM 508  
374 RRESAOKELLETLYGTKSCVPRWOTCISNTDDALGFALGSLFVATPDROSKETAEQM 433  
QY 509 ISEIRTAPEEALGOLVWDEKTRQAKKADAIYDMIGPPDIFLEKEILDVYDGEISE 568  
434 ISEIRTAPEEALGOLVWDEKTRQAKKADAIYDMIGPPDIFLEKEILDVYDGEISE 493  
QY 569 DSEFQNNMLVYNPSAVVMDOLRKPPSRDQSWTPTVAAVYLPTEKNEIVFPAGIIOAPE 628  
494 DSEFQNNMLVYNPSAVVMDOLRKPPSRDQSWTPTVAAVYLPTEKNEIVFPAGIIOAPE 553  
QY 629 YARNHPKALNFGGIGVWMEHELTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 688  
554 YARNHPKALNFGGIGVWMEHELTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 613  
QY 689 QYNQYVNGERLNGRQTIGENITDNGLKAAYNAYKAMLRKIGEEQOLPAVGLTNNQLPF 748  
614 QYNQYVNGERLNGRQTIGENITDNGLKAAYNAYKAMLRKIGEEQOLPAVGLTNNQLPF 673  
QY 749 VGEPAQWCSVRTPBESHEGLJNDPHSPARFVLGTLSNSRDLRHGCGVSGPMNGOIC 808  
674 VGEPAQWCSVRTPBESHEGLJNDPHSPARFVLGTLSNSRDLRHGCGVSGPMNGOIC 733  
QY 809 EYV 811  
734 EYV 736  
DB

RESULT 9  
US-09-999-832A-526  
Sequence 526, Application US/09999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Nejojeon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/085579  
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Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
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 QY 149 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGRSRNMTFNSLMDQNALIKHILENT 208  
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 QY 209 TFNSSSEAEOKTORFYLSCLQVERIEBELGAQPLRDLIEKIGWNITGPMQDNFMVYLKA 268  
 DB 134 TFNSSSEAEOKTORFYLSCLQVERIEBELGAQPLRDLIEKIGWNITGPMQDNFMVYLKA 193  
 QY 269 VAGTYATPFPFYVYISADSKSSNSNVIQVDSGLFLPSRDYLNRTANEKVLTAVIDYME 328  
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 QY 809 EYV 811  
 DB 734 EYV 736

RESULT 11  
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 ; Sequence 526, Application US/09978608A  
 ; Publication No. US20030045462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Geritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavitt, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C22  
 ; CURRENT APPLICATION NUMBER: US/09/978,608A  
 ; CURRENT FILING DATE: 2001-10-16  
 ; NUMBER OF SEQ ID NOS: 624  
 ; Prior Application removed - See File Wrapper or Palm  
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 ; LENGTH: 736  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-978-608A-526

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
 Best Local Similarity: 99.9%; Pred. No. 0;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGTROLLSGRTQLEVLVAGASLLAALLGCLVALGVQYHRDPSHSTCLTEACIRV 148  
 DB 14 VGFQKGTROLLSGRTQLEVLVAGASLLAALLGCLVALGVQYHRDPSHSTCLTEACIRV 73  
 QY 149 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGRSRNMTFNSLMDQNALIKHILENT 208  
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 DB 314 WLEFLSPLSPLSLDSEBPVVYVGM DYLOQVSELINRTEPSIINNYLINLVOKTSSLD 373  
 QY 449 RRESAOKELLETLYGKSKSCVRPMOTCISNTDDALGFALGSLFYKATPDRQSKETAEGM 508  
 DB 374 RRESAOKELLETLYGKSKSCVRPMOTCISNTDDALGFALGSLFYKATPDRQSKETAEGM 433  
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Db 554 YARNHFKALNFGGIGVWGHLELTHAFDDQREYDKENGLRPMWQNESLAFRNHTACMEB 613
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Db 614 QYNQYOVNBERLNGRQTLGENTLNDNGGLKAAVNAVYAMLRKKGEBQQLPAVGLTNHQLF 673
QY 749 VGEAOWWCSVRTPESSHEGLVTDPHSPARFVLTGTLNSRDFLRHGCPCVGSPPMNGQLC 808
Db 674 VGEAOWWCSVRTPESSHEGLVTDPHSPARFVLTGTLNSRDFLRHGCPCVGSPPMNGQLC 733
QY 809 EVW 811
Db 734 EVW 736

RESULT 12
US-09-978-585A-526
; Sequence 526, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavain, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978, 585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 526
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-526

Query Match 89.3%; Score 3824.5; DB 10; Length 736;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 434 ISIRTAFAFEALGOLVWMDKTRQAAKEKADAIYDMIGFPDFILPEKELDDVYDGEISE 493
QY 569 DSFFQNMNLNLYNSAKVMDOLRKPPSRDQMSMTPTQVNAVYLPPTNEIVFPAGIIQAPF 628
Db 494 DSFFQNMNLNLYNSAKVMDOLRKPPSRDQMSMTPTQVNAVYLPPTNEIVFPAGIIQAPF 553
QY 629 YARNHFKALNFGGIGVWGHLELTHAFDDQREYDKENGLRPMWQNESLAFRNHTACMEB 688
Db 554 YARNHFKALNFGGIGVWGHLELTHAFDDQREYDKENGLRPMWQNESLAFRNHTACMEB 613
QY 689 QYNQYOVNBERLNGRQTLGENTLNDNGGLKAAVNAVYAMLRKKGEBQQLPAVGLTNHQLF 748
Db 614 QYNQYOVNBERLNGRQTLGENTLNDNGGLKAAVNAVYAMLRKKGEBQQLPAVGLTNHQLF 673
QY 749 VGEAOWWCSVRTPESSHEGLVTDPHSPARFVLTGTLNSRDFLRHGCPCVGSPPMNGQLC 808
Db 674 VGEAOWWCSVRTPESSHEGLVTDPHSPARFVLTGTLNSRDFLRHGCPCVGSPPMNGQLC 733
QY 809 EVW 811
Db 734 EVW 736

RESULT 13
US-09-978-191A-526
; Sequence 526, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: us/09/978,191A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

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Query Match 89.3%; Score 3824.5; DB 10; Length 736;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 89 VGFQKGTROLLGSRTOELVLAGASLLALLLGLVAGVYHRDPSHSTCTEACIRV 148
DB 14 VGFQKGTROLLGSRTOELVLAGASLLALLLGLVAGVYHRDPSHSTCTEACIRV 73
QY 149 AGKILBSLDGRVSPCEPFYQFSCGCGWTRRNPDPGRSRMTFNSLMQNALIKHLENT 208
DB 74 AGKILBSLDGRVSPCEPFYQFSCGCGWTRRNPDPGRSRMTFNSLMQNALIKHLENT 133
QY 209 TFNSSSAEQKOTQRFYSCQVERIEELGAOPLRDLIEKIGNNITGPMQDNFMEYLKA 268
DB 134 TFNSSSAEQKOTQRFYSCQVERIEELGAOPLRDLIEKIGNNITGPMQDNFMEYLKA 133
QY 269 VAGTYRATPFYVYISADSKSSNSNVIOVDQSLFLPSRDYVYINRTANEKYLTAAYDYME 328
DB 194 VAGTYRATPFYVYISADSKSSNSNVIOVDQSLFLPSRDYVYINRTANEKYLTAAYDYME 253
QY 329 ELGMLTGRTRTSRECOQVLELEIOUANTVPODQDRDEKTYHKMSISELQALAPSD 388
DB 254 ELGMLTGRTRTSRECOQVLELEIOUANTVPODQDRDEKTYHKMSISELQALAPSD 313
QY 389 WLEFLSLPLSLELSDSEPVVYVGMVYIQVSELIINTEPSIANNYLIINLVOKTSSLD 448
DB 314 WLEFLSLPLSLELSDSEPVVYVGMVYIQVSELIINTEPSIANNYLIINLVOKTSSLD 373
QY 449 RRFESAQEKLETLVGTKSCVPRMOTCISNTD DALFALGSLFVKATPDROSKKEIAEGM 508
DB 374 RRFESAQEKLETLVGTKSCVPRMOTCISNTD DALFALGSLFVKATPDROSKKEIAEGM 433
QY 509 ISIRTPAFERALGOLVMMDEKTRQAAREKADATYDMIGFDPDILPELDDVYDGYISE 568
DB 434 ISIRTPAFERALGOLVMMDEKTRQAAREKADATYDMIGFDPDILPELDDVYDGYISE 493
QY 569 DSFFQNMALYNFSAKVMADQLRKPSRDQMSMTPTQVNAVYVLPKNEIVFPAGIILQAPF 628

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DB 494 DSFFQNMALYNFSAKVMADQLRKPSRDQMSMTPTQVNAVYVLPKNEIVFPAGIILQAPF 553
QY 629 YARNHPKALNFGGICGVYMGHELTTHAFDDQGREYDEKGNLRPMWQNESLAFNRHTACME 688
DB 554 YARNHPKALNFGGICGVYMGHELTTHAFDDQGREYDEKGNLRPMWQNESLAFNRHTACME 613
QY 689 QVNOYVNGERLNGRQTLGENTADNGGLKAAVNAVYKMLRKHGEQQLPAYGLTNHQLPF 748
DB 614 QVNOYVNGERLNGRQTLGENTADNGGLKAAVNAVYKMLRKHGEQQLPAYGLTNHQLPF 673
QY 749 VGFQVWCVRTPRESSHEGLVTDPHSPARFVYLGTLNSRDPLRHFGEVGSPPMNGQLC 808
DB 674 VGFQVWCVRTPRESSHEGLVTDPHSPARFVYLGTLNSRDPLRHFGEVGSPPMNGQLC 733
QY 809 EYW 811
DB 734 EYW 736

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## RESULT 14

US-09-978-403A-526

; Sequence 526, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerlitsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; PRIOR FILING DATE: 2002-03-19

; PRIOR FILING DATE: 2001-07-30

; PRIOR FILING DATE: 1997-10-17

; PRIOR FILING DATE: 1997-11-21

; PRIOR FILING DATE: 1997-11-03

; PRIOR FILING DATE: 1997-11-13

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; PRIOR FILING DATE: 1998-03-11

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; PRIOR FILING DATE: 1998-03-11

; PRIOR FILING DATE: 1998-03-11

; PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY VGRQKTRQLLGRSRTQELVLAGASLLALLLLGCVLAVGVHDPSSHSTCTTEACIRV 148  
DB VGRQKTRQLLGRSRTQELVLAGASLLALLLLGCVLAVGVHDPSSHSTCTTEACIRV 73  
QY AGKILSDRGVPCEDFYQFSCGGMIRRNPLPDGRSRNMTFSLMDONAILKHLLENT 208  
DB AGKILSDRGVPCEDFYQFSCGGMIRRNPLPDGRSRNMTFSLMDONAILKHLLENT 133  
QY TFNSSFBAEQKTORFYLSCLQVERIEELGAQPLRDLLEKIGWNITGPMQDNFMEYLKA 268  
DB TFNSSFBAEQKTORFYLSCLQVERIEELGAQPLRDLLEKIGWNITGPMQDNFMEYLKA 193  
QY VACTYRATPEFFTYTISADSSNSNVYQVQSGFLPBRDYINRTANKEVLTAYIDYME 328  
DB VACTYRATPEFFTYTISADSSNSNVYQVQSGFLPBRDYINRTANKEVLTAYIDYME 253  
QY ELGMLGCRPTSTREQMOVLELEIOLANITVPODORDEKTYHKMSISELOALAPSD 388  
DB ELGMLGCRPTSTREQMOVLELEIOLANITVPODORDEKTYHKMSISELOALAPSD 313  
QY WLEFLSLPLSELDSEPVVYVGMVYLQVSELINTEPSIINNYLIMVLVOKTTSSLD 448  
DB WLEFLSLPLSELDSEPVVYVGMVYLQVSELINTEPSIINNYLIMVLVOKTTSSLD 373  
QY RRESAOKELLETLYGFKSCVPRWQTCISNTDAGFALGSLFVKATPDRSKETIAEGM 508  
DB RRESAOKELLETLYGFKSCVPRWQTCISNTDAGFALGSLFVKATPDRSKETIAEGM 433  
QY ISSEIRTFEBALQOLVMDDEKTRQAAEKADAYIDMGFDFILEPELDDVDGYEISE 568  
DB ISSEIRTFEBALQOLVMDDEKTRQAAEKADAYIDMGFDFILEPELDDVDGYEISE 493  
QY DSFFQNNMLNINYSAKYVADQLRKPSPRQMSMTPTQVNAVYLPTKNEIVFPAGIIOAPF 628  
DB DSFFQNNMLNINYSAKYVADQLRKPSPRQMSMTPTQVNAVYLPTKNEIVFPAGIIOAPF 553  
QY YARNHPALNFGGIGVVMGHELTAFPDQGREYDKENGLPMMQNSLAFRNHTACME 668  
DB YARNHPALNFGGIGVVMGHELTAFPDQGREYDKENGLPMMQNSLAFRNHTACME 613  
QY QYNQYQVNGERLNGRQTLGEMNIDNGGLKAAVYNAKMLRKHGEEQOLPAVGLTNHQLFF 748  
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QY VGEPAQWCVSRTPBSSHGLVTDPHSPARFVIGTISNSDFLHFGCPVSGPMNPQOLC 808  
DB VGEPAQWCVSRTPBSSHGLVTDPHSPARFVIGTISNSDFLHFGCPVSGPMNPQOLC 733  
QY 809 EVW 811  
DB 734 EVW 736

RESULT 15  
US-09-978-564A-526  
Sequence 526, Application US/09978564A  
Publication No. US20030050241A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Raoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C25  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
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;; PRIOR APPLICATION NUMBER: 60/083559  
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;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
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;; PRIOR APPLICATION NUMBER: 60/084637  
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;; PRIOR APPLICATION NUMBER: 60/084640  
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;; PRIOR APPLICATION NUMBER: 60/085339  
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;; PRIOR APPLICATION NUMBER: 60/085338  
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;; PRIOR APPLICATION NUMBER: 60/085323  
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;; PRIOR APPLICATION NUMBER: 60/085582  
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;; PRIOR APPLICATION NUMBER: 60/085700  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGTROLLSRLTOLELVLAGASLLLAALLGCVLALGVGYHRDPSSHSTCLTEACIRV 148  
DB 14 VGFQKGTROLLSRLTOLELVLAGASLLLAALLGCVLALGVGYHRDPSSHSTCLTEACIRV 73

QY 149 AGKILESIDRGVSPCEDFYQSCGWIIRNPLPDGRSRNNTNSLMDQOAILIKHLENT 208  
DB 74 AGKILESIDRGVSPCEDFYQSCGWIIRNPLPDGRSRNNTNSLMDQOAILIKHLENT 133

QY 209 TNNSSSEAPQKTQRFYLSCLQVRIEELCAQPLRDILIEIKGNTTGPMDONFMEVLKA 268  
DB 134 TNNSSSEAPQKTQRFYLSCLQVRIEELCAQPLRDILIEIKGNTTGPMDONFMEVLKA 193

QY 269 VAGTYATPFTFYVYISADSKSSNSNVIQVDSGLFLPSBDYILNRPANKKVLJAYLDVME 328  
DB 194 VAGTYATPFTFYVYISADSKSSNSNVIQVDSGLFLPSBDYILNRPANKKVLJAYLDVME 253

QY 329 ELGMLGGRPTSTREMOQVLELEIOLANITVPQDRDEEKIYHMSISELQALAPSM 388  
DB 254 ELGMLGGRPTSTREMOQVLELEIOLANITVPQDRDEEKIYHMSISELQALAPSM 313

QY 389 WLEFLSFLSPLSLSDESVVYVYGYDYLQVSELINRTEPSILNNTYLLNVLVQKTTSSLD 448  
DB 314 WLEFLSFLSPLSLSDESVVYVYGYDYLQVSELINRTEPSILNNTYLLNVLVQKTTSSLD 373

Qy	449	RRPESAOEKLLETLVGTGKSCVPRMOTCI	NTDDALGFALGSLFVKATPDRQSKETAEGM	508		
Db	374	RRPESAOEKLLETLVGTGKSCVPRMOTCI	NTDDALGFALGSLFVKATPDRQSKETAEGM	433		
Qy	509	ISEIRTAFFEBALQOLVWMDKTRQA	AKEKADAIYDMIGFPDFILPEKELDDVYDYEISE	568		
Db	434	ISEIRTAFFEBALQOLVWMDKTRQA	AKEKADAIYDMIGFPDFILPEKELDDVYDYEISE	493		
Qy	569	DSFPQNNMLNYPFSAKVMADOLR	KPSRDQSMTPQTVNAYYLPTKNEIVFPAGILQAPF	628		
Db	494	DSFPQNNMLNYPFSAKVMADOLR	KPSRDQSMTPQTVNAYYLPTKNEIVFPAGILQAPF	553		
Qy	629	YARNHPKALNFGGIGVVMGHELTHA	FDQGREYDKEGNLRPMWQNESIAAFRNHTACMEZ	688		
Db	554	YARNHPKALNFGGIGVVMGHELTHA	FDQGREYDKEGNLRPMWQNESIAAFRNHTACMEZ	613		
Qy	689	QYNQYQVNGERLNGRQTLGENI	ADNGGLKAYNAYKAMLRKGEBQQLPAVGLTNHQLFF	748		
Db	614	QYNQYQVNGERLNGRQTLGENI	ADNGGLKAYNAYKAMLRKGEBQQLPAVGLTNHQLFF	673		
Qy	749	VGFPAQVWCSTVTPRESSHEGL	VTDPHSPARPRVLGTLNSRDFLRHGC	PVGS	PMNPGQLC	808
Db	674	VGFPAQVWCSTVTPRESSHEGL	VTDPHSPARPRVLGTLNSRDFLRHGC	PVGS	PMNPGQLC	733
Qy	809	EVW	811			
Db	734	EVW	736			

Search completed: July 3, 2004, 20:15:41  
Job time : 76 secs